

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	143.8	11.4	617	3	US-09-949-016-2369	Sequence 2369, App
2	51	4.0	11174	3	US-09-949-016-14111	Sequence 14111, A
3	48.6	3.9	30337	3	US-09-949-016-13053	Sequence 13053, A
4	45.4	3.6	1645	3	US-09-023-587A-5	Sequence 5, Appli
5	44.8	3.6	1053	3	US-09-902-540-2666	Sequence 2666, App
6	44.8	3.6	11558	6	PCT-US93-06251-23	Sequence 23, Appl
C 7	44.8	3.6	13706	3	US-09-902-540-1124	Sequence 1124, Ap
C 8	42.4	3.4	2133	3	US-09-902-540-4106	Sequence 4106, Ap
9	42.4	3.4	23738	3	US-09-902-540-1203	Sequence 1203, A
C 10	42	3.3	9622	3	US-09-949-016-15003	Sequence 15003, A
11	41.6	3.3	696	3	US-09-489-039A-3591	Sequence 3591, Ap
12	41	3.3	1097	3	US-09-771-161A-58	Sequence 58, Appl
13	41	3.3	3382	3	US-09-771-161A-59	Sequence 59, Appl
14	40.6	3.2	2943	3	US-09-902-540-3929	Sequence 3929, Ap
15	40.6	3.2	21295	3	US-09-902-540-1194	Sequence 1194, Ap
16	40.4	3.2	1533	3	US-09-902-540-7877	Sequence 7877, Ap
17	40.4	3.2	5228	3	US-09-902-540-789	Sequence 789, App
18	40.4	3.2	6651	3	US-09-902-540-4944	Sequence 4944, Ap
19	40.4	3.2	30780	3	US-09-902-540-1243	Sequence 1243, Ap
20	40.2	3.2	2802	3	US-09-949-016-1335	Sequence 1335, Ap
21	40.2	3.2	2806	3	US-09-688-188B-102	Sequence 102, App
22	40.2	3.2	2806	3	US-09-291-417D-102	Sequence 102, App
23	40.2	3.2	2838	3	US-09-949-016-794	Sequence 794, App
24	40.2	3.2	57559	3	US-09-949-016-13077	Sequence 13077, A

Db 251 CACCAAGACCTGCAGGATCTGTCTATCTTTCATCACCAATGTCACCTACCAACCTCGG 310
Qy 723 CCTTACACCTGCAATGTGTCGGGAGTTTGAGTTGAGCGCATCGGCCCTTTGTGAA 782
Db 311 CGACTACAGTGCACCGTCTACCGCTGCTCTTCTCGAAAACTACGAGCACAACCCAG 370
Qy 783 GACGACGGCTGATCCCTTAAGAGTCAACGAGGAGCTGAGAGGACTTCACCTCTGT 842
Db 371 CGTGTCAAGAGATCCATGTAGGTAGTGCACAAAGCCAAAGACATGGCATCAT 430
Qy 843 GGTCTCAAAATCATGATGATCATCTTCTGCTCTTCTTCTCAACCTGTGGTGTCTCATGA 902
Db 431 CGTGTCTGAGATCATGATGATGCTCATTTGTGTTGACCATATATGGCTCGTGGCAGA 490
Qy 903 GATGATATATTGCTACAGAAAGTCTCAAAAGCCGAAGAG---CGAGCCCAAGAAAGCC 959
Db 491 GATGATTTACTGCTACAGAAAGATCGCTGCGGCCCAACGAGACTCTGCACAGGAGATGC 550
Qy 960 GTCTGACTACCTTGCCATCCCATCTTGAGAACCAAGAGAACTCTCGGG 1006
Db 551 CTCGAATACTGCGCATCACCTCTGAAAGCAAGAGAACTGCAAGG 597

RESULT 2

US-09-949-016-14111
; Sequence 14111, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14111
; LENGTH: 11174
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(11174)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14111

Query Match 4.0%; Score 51; DB 3; Length 11174;
Best Local Similarity 58.1%; Pred. No. 0.0045;
Matches 90; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
Qy 441 CTTCCTCTGTGTGTGGAAGTCCCTCGAGACGAGGCGGTGACAGGCAACCCCATGAA 500
Db 2011 CTCGGGGGCTGCGTGGAGGTGGAATCGAGACCGAGGCGGTGTATGGATGACCTTCAA 2070
Qy 501 GCTGCGCTGCATCTCTCATGAAGAGAGAGGAGTGGAGGCCACCGGTGGTGAATG 560
Db 2071 AATTTCTTTCATCTCTCTGAAGCGCCGAGCGAGACCAACGCTGAGACCTTCACCGAGTG 2130
Qy 561 GTTCTACAGGCCGAGCGGCGGTAAAGATTTTCCTTA 595
Db 2131 GACCTTCGCCAGAGAGGCACTGAGAGTTTGTCA 2165

RESULT 3

US-09-949-016-13053
; Sequence 13053, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13053
; LENGTH: 30337
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(30337)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13053

Query Match 3.9%; Score 48.6; DB 3; Length 30337;
Best Local Similarity 63.0%; Pred. No. 0.028;
Matches 75; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Qy 829 GACTTCACCTCTGTGGTCTCAGAAATCATGATGATCATCTTCTGTGTTCTTCTCACCTG 888
Db 620 GACATGCGATCCATCGTCTGAGATCATGATGATGCTCATTTGTTGTTGACCAT 679
Qy 889 TGGTGTCTCATTCGAGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAAGGCGAGC 947
Db 680 TGGCTCGTGGCAGAGATGATTTACTGCTACAGAAAGATCGTGCAGCGCAGAGACTGC 738

RESULT 4

US-09-023-587A-5
; Sequence 5, Application US/09023587A
; Patent No. 6653530
; GENERAL INFORMATION:
; APPLICANT: Shewmaker, Christine K.
; APPLICANT: Bhat, Ganesh B.
; APPLICANT: Venkatramesh, Mylavarapu
; APPLICANT: Rangwala, Shaikat H.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Boddupalli, Sekhar S.
; TITLE OF INVENTION: Methods for Producing Carotenoid Compounds, Tocopherol Compounds,
; Specialty Oils in Plant Seeds
; FILE REFERENCE: 16516.122
; CURRENT APPLICATION NUMBER: US/09/023,587A
; CURRENT FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1645
; TYPE: DNA
; ORGANISM: Zea mays
US-09-023-587A-5

Query Match 3.6%; Score 45.4; DB 3; Length 1645;
Best Local Similarity 46.2%; Pred. No. 0.068;
Matches 151; Conservative 0; Mismatches 176; Indels 0; Gaps 0;
Qy 429 GGTGAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGGAGACGGAGGCCGTGCAGGG 488
Db 349 GGTGTCAACGGCTCTTCTTAAAGTACGAGGCCGCCCAAGAGCGGCTGTACGT 408
Qy 489 CAACCCCATGAAGCTGCGCTGCATCTCTCTGATCAAGAGAGAGGAGGTGGAGGCCACAC 548
Db 409 GGTGCACTTACAACTACGACGCGAGCAACGCGCAAGTTCGCGCGCGAGAACGCGTCTGTT 468

Db 4948 GACITCTCCAGGACCTGGTGGACCTGGCTCGAAGATGACGGACGGGAGCGGCACCTC 4889
Qy 496 ATGAGCTGCGCTGCATCTCTGCATGAAGAGAGGAGGTGGAGGCCACACCGTGGTG 555
Db 4888 ATCCACCGCGCTGGTGGCTTCTTCGCGACGGGTGACAGCATCTGTCGGCAACAACTGGTG 4829
Qy 556 GAATGGTTCTACAGGCCCGGAGGGCGGTAAAGATTTTCCTTTATTACGAGTATCGGAATGGC 615
Db 4828 CTGAACCTCTACAGCACTGAAGCCCTGAGGGCGGATGTAACCTGTCCGCGCAGCTC 4769
Qy 616 CACGAGGAGGTG 627
Db 4768 TACGAGGAGCG 4757

RESULT 8
US-09-902-540-4106/c
; Sequence 4106, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4106
; LENGTH: 2133
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4106

Query Match 3.4%; Score 42.4; DB 3; Length 2133;
Best Local Similarity 51.6%; Pred. No. 0.46; Mismatches 91; Indels 0; Gaps 0;
Matches 97; Conservative 0;
Qy 462 GCCCTCGGAGCGGAGCGCGTGCAGGGCAACCCCATGAAGCTGCGCTGCATCTCTGCAT 521
Db 1813 GGCCAGGATGATGGCGGGCGCCATCCGTTGGAAGACGGGTGCAAGCGCGCTGCAG 1754
Qy 522 GAAGAGAGAGGTGGAGGCCACACCGTGTGGAATGTTTACAGGCCCGCGAGGGCGG 581
Db 1753 GAAAGCGGGCGGAGTGGGACACGCTGGGCGTGGGACCGCTTCCACGACCATGTGCT 1694
Qy 582 TAAAGATTCTTATTACGAGTATCGGAATGGCCACGAGGTGGAGAGCCCTTTCA 641
Db 1693 GGGTGAAGGCTCCGCTAGAGGATCTGCGGGAATCTCCAGCTCGGACAGCGCGCGTCA 1634
Qy 642 GGGGCGCC 649
Db 1633 GCTCCGCC 1626

RESULT 9
US-09-902-540-1203
; Sequence 1203, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1203
; LENGTH: 23738
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1203
Query Match 3.4%; Score 42.4; DB 3; Length 23738;
Best Local Similarity 51.6%; Pred. No. 1.1; Mismatches 91; Indels 0; Gaps 0;
Matches 97; Conservative 0;
Qy 462 GCCCTCGGAGCGGAGCGCGTGCAGGGCAACCCCATGAAGCTGCGCTGCATCTCTGCAT 521
Db 4191 GGCCAGGATGATGGCGGGCGCCATCCCGTTGGAAGACGGTGCAGCGCGCTGCAG 4250
Qy 522 GAAGAGAGAGGTGGAGGCCACCGCTGAGGATGTTTACAGGCCCGAGGGCGG 581
Db 4251 GAAAGCGGGCGGAGTGGGACACGCTGGGCGTGGGACCGCTTCCAGACCATGTGCTG 4310
Qy 582 TAAAGATTCTTATTACGAGTATCGGAATGGCCACGAGGTGGAGAGCCCTTTCA 641
Db 4311 GGGTGAAGCGCTCCGCTACGAGGATCTGCGGGAATCTCCAGTCCGACGCGCGTCA 4370
Qy 642 GGGGCGCC 649
Db 4371 GCTCCGCC 4378

RESULT 10
US-09-949-016-15003/c
; Sequence 15003, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15003
; LENGTH: 9622
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15003
Query Match 3.3%; Score 42; DB 3; Length 9622;
Best Local Similarity 49.5%; Pred. No. 0.99; Mismatches 108; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
Qy 38 GAGCAGGACGAGCGCGGAGTGGAGTTCGGGGTGGCGGGAGCGGAGCTGTC 97
Db 7138 GCGTGAGGCCCTGTGGAAGGGGTGCGTCTGCCGTAGGGGCTCTGTTCCATGCCACGA 7079
Qy 98 CGTGTGCTGAGCGCCGCGGAGAGCGCGCGGAGCGGCTGATCGGCTCCCTCGAAGTGG 157
Db 7078 TCTGCTGCTGTTGGGGCCAGCGCGGTGTAGGAAGCATCATGCCCTCCATCGGCTGG 7019
Qy 158 GGAGGTCCAGTGGGTGCTTAGGGCCCAAGCCCCCAGCCCGGCTCCAAAGCTCCACAG 217
Db 7018 ACAGGACCTCTGGGGGACAGTGAAGCTTACCCCGCTGGCTGTCCACGCGCTCCACG 6959
Qy 218 GCCTCCCGAGCAGCGGTGCTCGGCCCTTCCCTTCGCTC 255
Db 6958 TACACCCGAGCAGCCTCCCTTCTGATCTCTTGGGAC 6921

RESULT 11
US-09-489-039A-3591
; Sequence 3591, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3591
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3591

Query Match 3.3%; Score 41.6; DB 3; Length 696;
Best Local Similarity 48.3%; Pred. No. 0.5;
Matches 116; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

Qy 458 AAGTGCCCTCGGACAGGAGCGGTGAGGCCACCGCGTGGTGAATGTTCTACAGGCCCGAGG 577
Db 92 AGGCGCGGACGTGCGGACGCGGTGCTGGGCAAGCTGCCGAAGCCGCGCTATGCCGACT 151

Qy 518 GCATGAAGAGAGAGAGGTGAGGCCACCGCGTGGTGAATGTTCTACAGGCCCGAGG 577
Db 152 ACCTGCCGTTCAACGACGTTGACGTTACCGCGCTGGATCAGGGGATTCGCTGTTCC 211

Qy 578 GCGTAAAGATTTCCTATTACAGTATCGGAATGCCACAGAGGTGAGAGCCCT 637
Db 212 CCGGCGCGAATCTCTTTACCGGGAAGATGTGTTAGCTGACGGGCCACGCGGCCCGG 271

Qy 638 TTCAGGGCGCTCGAGTGAATGCGACAGGACCTGCGAGGAGTGTCCATCACTGTC 697
Db 272 TCATTCTGACCTGCTGCTTAAAGTATTCTGACCCCTGCCGGCGCTCGGATCCGAGG 331

RESULT 12
US-09-771-161A-58
; Sequence 58, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 58
; LENGTH: 1097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-161A-58

Query Match 3.3%; Score 41; DB 3; Length 1097;
Best Local Similarity 52.0%; Pred. No. 0.84;
Matches 92; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 1 CCCTCCCTTCGAGCTGAGCTTACCTCGGCGCAACAGCAGGCGCGGCGAGTGG 60

Db 23 CCCCCGGCTCGGGGCTGTGAGCGGCTCGGGGCCCGGGGCTGGGCGGCGGTGCGGCGGGCGG 82
Qy 61 AAGCTGGAGTTCCGGGGTGGGCGGAGGAGCACTGTCCGTGGTGTCTGAGGCGCGGCGGAGA 120
Db 83 CCGACGCTCTCTTCGGCGGCGGCGGCGGCGCATCGTGGGGCGGCGCGGCTGGGGCG 142
Qy 121 GCGGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCTAGTGGGGTCCGT 177
Db 143 GCCGGCGCGAGTTGCTCCCGGGGCGCGGCTGAGGGCCCCCGCGCGCGCGCT 199

RESULT 13
US-09-771-161A-59
; Sequence 59, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 59
; LENGTH: 3382
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: -
; LOCATION: (1)..(3382)
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'
US-09-771-161A-59

Query Match 3.3%; Score 41; DB 3; Length 3382;
Best Local Similarity 52.0%; Pred. No. 1.3;
Matches 92; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 1 CCCTCCCTTCGAGCTGAGCTTACCTCGGCGCAACAGCAGGCGCGGCGAGTGG 60
Db 23 CCCCCGGCTCGGGGCTGTGAGCGGCTCGGGCGGGGGTGGCGGCTGCGGCGGGCGG 82
Qy 61 AAGCTGGAGTTCCGGGGTGGGCGGAGGAGCACTGTCCGTGGTGTCTGAGGCGGCGGAGA 120
Db 83 CCGACGCTCTCTTCGGCGGCGGCGGCGGCGCATCGTGGGGCGGCGGCGGCTGGGGCG 142
Qy 121 GCGGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCTAGTGGGGTCCGT 177
Db 143 GCCGGCGCGAGTTGCTCCCGGGGCGCGGCTGAGGGCCCCCGCGCGCGCGCT 199

RESULT 14
US-09-902-540-3929
; Sequence 3929, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3929

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; LENGTH: 2943
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3929

Query Match          3.2%; Score 40.6; DB 3; Length 2943;
Best Local Similarity 48.9%; Pred. No. 1.5;
Matches 109; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 460 GTGCCCTCGGAGACGAGGCGGTGCAGGGCAACCCATGAAGCTGCGCTGCATCTCCTGC 519
    |||||
Db 1831 GTGCTGGAAGAGTGGAGCGCGGTGCGCGAGCTGGCGCTGATGCCCGGAGGCCGCG 1890
    |||||

QY 520 ATGAAGAGAGAGGAGTGGAGGCCACACACGCTGTGTGGAATGTTCTACAGGCCCGAGGGC 579
    |||||
Db 1891 ATGGCTACGCGCAGAGACTGAAGCCCGCTGGAGGCGCGCGCCACAGGTGAAGCGC 1950
    |||||

QY 580 GGTAAGATTTCCTTATTACAGATATCGGAATGGCCACAGAGGTTGAGAGCCCTTT 639
    |||||
Db 1951 GCCTATGACCCGCTCCTGGACGTGGCAGCTTCGACCGCCCGCGGTGGAGCGCTGGTG 2010
    |||||

QY 640 CAGGGGCCCTGCACTGAATGGCAGCAAGACCTGCAGGAGC 682
    |||||
Db 2011 AAGCGGCCAGGAGCGCATGGGCATCGAGGCCGACGAGGAGG 2053
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RESULT 15
US-09-902-540-1194
; Sequence 1194, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1194
; LENGTH: 21295
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1194
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Query Match          3.2%; Score 40.6; DB 3; Length 21295;
Best Local Similarity 48.9%; Pred. No. 3.1;
Matches 109; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 460 GTGCCCTCGGAGACGAGGCGGTGCAGGGCAACCCATGAAGCTGCGCTGCATCTCCTGC 519
    |||||
Db 2609 GTGCTGGAAGAGTGGAGCGCGGTGCGCGAGCTGGCGCTGATGCCCGGAGGCCGCG 2668
    |||||

QY 520 ATGAAGAGAGAGGTTGAGGCCACACGCTGTGTGGAATGTTCTACAGGCCCGAGGGC 579
    |||||
Db 2669 ATGGCTACGCGCAGAGCTGAAGCCCGCTGGAGGCGCGCGCCACAGGTGAAGCGC 2728
    |||||

QY 580 GGTAAGATTTCCTTATTACAGATATCGGAATGGCCACAGAGGTTGAGAGCCCTTT 639
    |||||
Db 2729 GCCTATGACCCGCTCCTGGACGTGGCAGCTTCGACCGGCCCGCGGTGGAGCGCTGGTG 2788
    |||||

QY 640 CAGGGCGCGCTCAGTGGAAATGGCAGCAAGGACCTGCAGGAGC 682
    |||||
Db 2789 AAGCGGCCAGGAGCGCATGGGCATCGAGGCCGACGAGGAGG 2831
    |||||
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Search completed: December 13, 2005, 07:35:09
Job time : 295.5 secs

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 07:13:57 ; Search time 1440 Seconds
(without alignments)
7241.448 Million cell updates/sec

Title: US-09-977-579a-4
Perfect score: 1261
Sequence: 1 cctcccttcgagctgagc.....tgcagaaactgagaagccgg 1261

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Maximum DB seq length: 2000000000

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Maximum Match 100%

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8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1261	100.0	1261	3	US-09-977-579a-4
2	1259.4	99.9	1261	9	US-10-482-834A-22
3	600	47.6	600	10	US-11-060-756-2816
4	600	47.6	600	10	US-11-060-756-2817
5	600	47.6	600	10	US-11-060-756-7088
6	600	47.6	600	10	US-11-060-756-7089
7	561.8	44.6	1195	9	US-10-450-763-22568
8	559.6	44.4	2632	5	US-10-029-191-22
9	559.6	44.4	3108	5	US-10-029-191-1
10	540	42.8	2220	3	US-09-977-579-3
11	534.6	42.4	645	5	US-10-029-191-21
12	416	33.0	651	4	US-09-925-065A-513769
13	415.6	33.0	651	4	US-09-925-065A-513767
14	415.6	33.0	651	4	US-09-925-065A-513768
15	392.6	31.1	3531	9	US-10-450-763-22567
16	225.2	18.2	545	4	US-09-925-065A-774904
17	224.4	17.8	621	9	US-10-450-763-22566
18	216	17.1	4625	3	US-09-764-891-7659
19	148.2	11.8	657	5	US-10-029-191-23
20	143.8	11.4	1275	10	US-11-060-756-3901
21	143.8	11.4	1275	10	US-11-060-756-8173
22	143.8	11.4	1335	8	US-10-723-860-2247
23	142.2	11.3	1414	8	US-10-477-272-1
					Sequence 4, Appli
					Sequence 22, Appl
					Sequence 2816, Ap
					Sequence 7088, Ap
					Sequence 7089, Ap
					Sequence 22568, A
					Sequence 22, Appl
					Sequence 1, Appli
					Sequence 3, Appli
					Sequence 513769,
					Sequence 513767,
					Sequence 513768,
					Sequence 22567, A
					Sequence 774904,
					Sequence 22566, A
					Sequence 7659, Ap
					Sequence 23, Appl
					Sequence 3901, Ap
					Sequence 8173, Ap
					Sequence 2247, Ap
					Sequence 1, Appli

RESULT 1

US-09-977-579a-4

; Sequence 4, Application US/09977579

; Publication No. US20040248240A1

; GENERAL INFORMATION:

; APPLICANT: Cambridge University Technical Services

; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod

; TITLE OF INVENTION: channel

; FILE REFERENCE: 674558-2001

; CURRENT APPLICATION NUMBER: US/09/977,579

; PRIOR FILING DATE: 2001-10-15

; PRIOR FILING DATE: 2000-02-24

; PRIOR FILING DATE: 2000-02-24

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 1261

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-977-579a-4

Query Match	100.0%;	Score 1261;	DB 3;	Length 1261;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1261;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	CCCTCCCTTCGAGCTCAGCTTACCTCTGGGCGCAAAACGAGCGAGGCGCGGAGTGG 60		
Db	1	CCCTCCCTTCGAGCTCAGCTTACCTCTGGGCGCAAAACGAGCGAGGCGCGGAGTGG 60		
Qy	61	AAGCTGAGTTCGGGGTGGGCGGAGGCGGAGTCCGCTGCTGCTGAGCCCGCGGAGA 120		
Db	61	AAGCTGAGTTCGGGGTGGGCGGAGGCGGAGTCCGCTGCTGCTGAGCCCGCGGAGA 120		
Qy	121	CGCGGCGGAGCGGCTGATCGGCTCCCTCGAACTCGGGGAGGTCAGTGGGGTTCGCTTAG 180		
Db	121	CGCGGCGGAGCGGCTGATCGGCTCCCTCGAACTCGGGGAGGTCAGTGGGGTTCGCTTAG 180		
Qy	181	GGCCCCAAGCCCCACCCCGCTCCAAAGTCTCCAGGGCTCCCGAGCACCGGTGCTCG 240		
Db	181	GGCCCCAAGCCCCACCCCGCTCCAAAGTCTCCAGGGCTCCCGAGCACCGGTGCTCG 240		
Qy	241	GCCTTCCTTCGCTCAGAAAGTCCCGCTGGGGGAGTTCGTCCTCCAAAGGTTCTCTCG 300		
Db	241	GCCTTCCTTCGCTCAGAAAGTCCCGCTGGGGGAGTTCGTCCTCCAAAGGTTCTCTCG 300		

ALIGNMENTS

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Db 241 GCCCTTCTCTCGTCAGAAAGTCGCCCTCGGGGCGAGTTCTGTCCTCCAAAGAGGTTTCTCTCG 300
Qy 301 AAAGAATCTGAGAGGCGCAGTCCTTGACCGAGGGAATCTCTGTGTAGCCTTGGAGC 360
Db 301 AAAGAATCTGAGAGGCGCAGTCCTTGACCGAGGGAATCTCTGTGTAGCCTTGGAGC 360
Qy 361 GCCAGAGCCCAAGAGATGCCCTTCAATAGATTGTTTCCCTCGGCTTCTCTGTGCTT 420
Db 361 GCCAGAGCCCAAGAGATGCCCTTCAATAGATTGTTTCCCTCGGCTTCTCTGTGCTT 420
Qy 421 ATCTACTGGGTCAAGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGAGACGAGGCC 480
Db 421 ATCTACTGGGTCAAGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGAGACGAGGCC 480
Qy 481 GTGAGGCAACCCCATCAAGCTGCGTCATCTCTGCATGAAGAGAGAGGAGGTGGAG 540
Db 481 GTGAGGCAACCCCATCAAGCTGCGTCATCTCTGCATGAAGAGAGAGGAGGTGGAG 540
Qy 541 GCCACACGGTGGTGAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTATAC 600
Db 541 GCCACACGGTGGTGAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTATAC 600
Qy 601 GAGTATCGGAATGGCCACAGAGGTGAGAGCCCTTTTCAGGGGCGCTCGAGTGAAT 660
Db 601 GAGTATCGGAATGGCCACAGAGGTGAGAGCCCTTTTCAGGGGCGCTCGAGTGAAT 660
Qy 661 GGCAGCAGGACCTGCAGAGCGTGCATCACTGTCTCAAGCTCACTCTGAACGACTCT 720
Db 661 GGCAGCAGGACCTGCAGAGCGTGCATCACTGTCTCAAGCTCACTCTGAACGACTCT 720
Qy 721 GGCCTCTACACTGCAATGTGTCCCGGAGTTTGAGTTTGAGGGCGATCGGCCCTTTGTG 780
Db 721 GGCCTCTACACTGCAATGTGTCCCGGAGTTTGAGTTTGAGGGCGATCGGCCCTTTGTG 780
Qy 781 AAGACGACCGGCTGATCCCCCTAAGAGTCAACGAGGAGGTGAGAGGACTTCACTCT 840
Db 781 AAGACGACCGGCTGATCCCCCTAAGAGTCAACGAGGAGGTGAGAGGACTTCACTCT 840
Qy 841 GTGGTCTCAGAAATCATGATGATATCTTCTGTGCTTCTCCTCACCTGTGCTCTCATC 900
Db 841 GTGGTCTCAGAAATCATGATGATATCTTCTGTGCTTCTCCTCACCTGTGCTCTCATC 900
Qy 901 GAGATGATATATTTGTACAGAAAGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGCG 960
Db 901 GAGATGATATATTTGTACAGAAAGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGCG 960
Qy 961 TCTGACTACCTTGGCATCCCATCTGAGAAACAAGAGAACTCTGCGGTACCAAGTGAAGAA 1020
Db 961 TCTGACTACCTTGGCATCCCATCTGAGAAACAAGAGAACTCTGCGGTACCAAGTGAAGAA 1020
Qy 1021 TAGACAGGACGAGTGCATGAGTGGCTGACACCTGAGGACCTGGACATCCCATG 1080
Db 1021 TAGACAGGACGAGTGCATGAGTGGCTGACACCTGAGGACCTGGACATCCCATG 1080
Qy 1081 TTCAGCAATGTCATGGCATCAGAGGCGGCCCAAGGGGCCCATCGCTTCCCTTCATGC 1140
Db 1081 TTCAGCAATGTCATGGCATCAGAGGCGGCCCAAGGGGCCCATCGCTTCCCTTCATGC 1140
Qy 1141 ATCCATTTCTGTGTCATTCATTCATCATATCCATCCATCCCTCTGAGCTTTTCACTCT 1200
Db 1141 ATCCATTTCTGTGTCATTCATTCATCATATCCATCCATCCCTCTGAGCTTTTCACTCT 1200
Qy 1201 GACTCCCTTAACCTCCATGAGCTCTACCGACCATTAAGACTTGGCCAGAACTGAGAGCGC 1260
Db 1201 GACTCCCTTAACCTCCATGAGCTCTACCGACCATTAAGACTTGGCCAGAACTGAGAGCGC 1260
Qy 1261 G 1261
Db 1261 G 1261
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RESULT 2

US-10-482-834A-22

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; Sequence 22, Application US/10482834A
; Publication No. US20050074764A1
; GENERAL INFORMATION:
; APPLICANT: Mulley, John Charles
; APPLICANT: Harkin, Louise Anne
; APPLICANT: Dibbens, Michelle
; APPLICANT: Wallace, Robyn
; APPLICANT: Phillips, Hillary Anny
; APPLICANT: Heron, Sara Elizabeth
; APPLICANT: Berkovic, Samuel Frank
; APPLICANT: Scheffer, Ingrid Bileen
; APPLICANT: Biomedics Limited
; TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
; FILE REFERENCE: 1386/17
; CURRENT APPLICATION NUMBER: US/10482,834A
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-482-834A-22
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Query Match 99.9%; Score 1259.4; DB 9; Length 1261;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CCCTCCCTTCGAGCTGAGCTTACCCTGGCGCAAAACGAGCGAGGCGAGGCGGAGTGG 60
Db 1 CCCTCCCTTCGAGCTGAGCTTACCCTGGCGCAAAACGAGCGAGGCGAGGCGGAGTGG 60
Qy 61 AAGCTGAGTTCGGGGTGGCGGAGGCGAGCTGCTCCGTGCTGCTGAGCCCGCGGAGA 120
Db 61 AAGCTGAGTTCGGGGTGGCGGAGGCGAGCTGCTCCGTGCTGCTGAGCCCGCGGAGA 120
Qy 121 GCGGGCGGAGCGGCTGATCGCTCCCTGAACTGGGAGGTCACAGTGGGGTCCCTTAG 180
Db 121 GCGGGCGGAGCGGCTGATCGCTCCCTGAACTGGGAGGTCACAGTGGGGTCCCTTAG 180
Qy 181 GGCCCAAAGCCCCACCCGGCTCCAAAAGTCCCAAGGCTCCCAAGGCTCCCAAGGCTCC 240
Db 181 GGCCCAAAGCCCCACCCGGCTCCAAAAGTCCCAAGGCTCCCAAGGCTCCCAAGGCTCC 240
Qy 241 GCCCTTCCTTCGTCAGAAAGTCCGCCCTGGGGGAGTTCGTCCTCCAAAGAGGTTTCTCTCG 300
Db 241 GCCCTTCCTTCGTCAGAAAGTCCGCCCTGGGGGAGTTCGTCCTCCAAAGAGGTTTCTCTCG 300
Qy 301 AAAGAACTGAGAGGCGCAGTCTTGACCGAGGGAATCTCTGTGTAGCCTTGGAGC 360
Db 301 AAAGAACTGAGAGGCGCAGTCTTGACCGAGGGAATCTCTGTGTAGCCTTGGAGC 360
Qy 361 CGCCAGCCCCAGAAAGATGCTTCCCTTCAATAGATTGTTTCCCTCGGCTTCTCTGTGCTT 420
Db 361 CGCCAGCCCCAGAAAGATGCTTCCCTTCAATAGATTGTTTCCCTCGGCTTCTCTGTGCTT 420
Qy 421 ATCTACTGGTTCAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGAGACGAGGCC 480
Db 421 ATCTACTGGTTCAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGAGACGAGGCC 480
Qy 481 GTGAGGCAACCCCATCAAGCTGCGTCATCTCTGCATGAAGAGAGAGAGGAGGTGGAG 540
Db 481 GTGAGGCAACCCCATCAAGCTGCGTCATCTCTGCATGAAGAGAGAGAGGAGGTGGAG 540
Qy 541 GCCACCAAGTGTGGAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTATAC 600
Db 541 GCCACCAAGTGTGGAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTATAC 600
Qy 601 GAGTATCGGAATGGCCACAGAGGTGAGAGCCCTTTTCAGGGGCGCTCGAGTGAAT 660
Db 601 GAGTATCGGAATGGCCACAGAGGTGAGAGCCCTTTTCAGGGGCGCTCGAGTGAAT 660
Qy 661 GGCAGCAGGACCTGCAGGACGTCATCACTGTCTCAAGCTCACTCTGAACGACTCT 720
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Db	661	GGCAGCAAGGACCTGCGAGGCGTGTGCATCACTGTCTCAACGTCATCTCGAACGACTCT	720
Qy	721	GGCCTCTACACCTGCAATGTGTCCCGGAGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTG	780
Db	721	GGCCTCTACACCTGCAATGTGTGTCCCGGAGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTG	780
Qy	781	AAGACGACGGCGTGATCCCCCTAAGAGTCAACGAGGAGGCTGAGAGGACTTCACCTCT	840
Db	781	AAGACGACGGCGTGATCCCCCTAAGAGTCACTGAGGAGGCTGAGAGGACTTCACCTCT	840
Qy	841	GTGGTCTCAGAAATCATGATGATCATCTCTCGTCTTCTCTCAACCTGTGGCTGCTCATC	900
Db	841	GTGGTCTCAGAAATCATGATGATCATCTCTCTGTCTTCTCTCACCTGTGGCTCATC	900
Qy	901	GAGATGATATATTGCTACAGAAAGGTCTCAAAGCCGAAGGCGAGGCCCAAGAAAACGCG	960
Db	901	GAGATGATATATTGCTACAGAAAGGTCTCAAAGCCGAAGGCGAGGCCCAAGAAAACGCG	960
Qy	961	TCTGACTACCTTGGCCATCCCATCTGAGAAACAAAGAGAGAACTCTGCGGTACCAAGTGAGAGAA	1020
Db	961	TCTGACTACCTTGGCCATCCCATCTGAGAACAAAGGAGAGAACTCTGCGGTACCAAGTGAGAGAA	1020
Qy	1021	TAGAACAGGAGCAGTGTGACATGAGGTGGCCTGAAACAACCTGAGGGAATGAGCATCCCATG	1080
Db	1021	TAGAACAGGAGCAGTGTGACATGAGGTGGCCTGAAACACCTGAGGGAATGAGCATCCCATG	1080
Qy	1081	TTGACGAATGTCAATGTCATCAGAGAGGCGGCCCAAGGGCCCCATCGCTTCCCTTTATGC	1140
Db	1081	TTGACGAATGTCAATGTCATCAGAGAGGCGGCCCAAGGGCCCCATCGCTTCCCTTTATGC	1140
Qy	1141	ATCATTTGTTCTGTTTCATTCATCCATATCCACCTGCGCTCTGAGCTTTCACTCT	1200
Db	1141	ATCATTTGTTCTGTTTCATTCATTCATCCATATCCACCTGCGCTCTGAGCTTTCACTCT	1200
Qy	1201	GACTTCCCTTAATCCATCAGACCTCTACGCAACCAAGACTCTGCGAGACTGAGAGCCG	1260
Db	1201	GACTTCCCTTAATCCATCAGACCTCTACGCAACCAAGACTCTGCGAGACTGAGAGCCG	1260
Qy	1261	G 1261	
Db	1261	G 1261	

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RESULT 3
US-11-060-756-2816
; Sequence 2816, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2816
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2816

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	Query Match	47.6%	Score 600	DB 10	Length 600
Best Local Similarity	100.0%				
Matches 600	Conservative 0	Mismatches 176			
			Indels 0	Gaps 0	
Qy	662	GCACGAAGGACCTCAGGAGCTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTG	721		
Db	1	GCACGAAGGACCTCAGGAGCTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTG	60		
Qy	722	GCCTCTACACCTGCACATGTGTCCCGGAGTTTGTAGTTTGAGCGGCATCGGCCCTTCTGTGA	781		

Db	61	GCCTCTACACCTGCAATGTGTCCGGGAGTTTGAGTTTGGGGCGCATCGGCCCTTTGTGA	120
Qy	782	AGACGACGGCGGTGATCCCCCTTAAGAGTCAACCGAGGAGGCTGGAGAGGACTTCACCTCTG	841
Db	121	AGACGACGGCGGTGATCCCCCTTAAGAGTCAACCGAGGAGGCTGGAGAGGACTTCACCTCTG	180
Qy	842	TGGFTCTCAGAAATCATGATGATGATCATCTTCTGGFTTTCCTCAACCCCTGTGGCTGCTCATCG	901
Db	181	TGGFTCTCAGAAATCATGATGATGATGATCATCTTCTGGFTTTCCTCAACCCCTGTGGCTGCTCATCG	240
Qy	902	AGATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAGGAGGCGAGCCCAAGAAACCGGT	961
Db	241	AGATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAGGAGGCGAGCCCAAGAAACCGGT	300
Qy	962	CTGACTACCTTGGCCATCCCATCTGAGAAACAAGAGAACTCTGGGGTACCAGTGGAGGAAT	1021
Db	301	CTGACTACCTTGGCCATCCCATCTGAGAAACAAGAGAACTCTGGGGTACCAGTGGAGGAAT	360
Qy	1022	AGAACGAGGAGGTGTGACATGATGAGTGGCTCTGAACACCTGAGGGAATGGACATCCCATGT	1081
Db	361	AGAACGAGGAGGTGTGACATGATGAGTGGCTCTGAACACCTGAGGGAATGGACATCCCATGT	420
Qy	1082	TCAGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCCATCGCTTCCCTTCATGCA	1141
Db	421	TCAGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCCATCGCTTCCCTTCATGCA	480
Qy	1142	TCCATTGTTCTGTTTCATTTCATTCATCATACATCCACCTCGCTCTGAGCTTTCACCTCTG	1201
Db	481	TCCATTGTTCTGTTTCATTTCATTCATCATACATCCACCTCGCTCTGAGCTTTCACCTCTG	540
Qy	1202	ACTCCCTAACTCCATCAGACCTCTACGACCAATAAGACTCTGCCAGAACTGAGAAAGCCGG	1261
Db	541	ACTCCCTAACTCCATCAGACCTCTACGACCAATAAGACTCTGCCAGAACTGAGAAAGCCGG	600
RESULT 4			
US-11-060-756-2817			
; Sequence 2817, Application US/11060756			
; Publication No. US20050221354A1			
; GENERAL INFORMATION:			
; APPLICANT: Wyeth			
; APPLICANT: Mounts, William Martin			
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles o			
; TITLE OF INVENTION: Target Genes			
; FILE REFERENCE: AM101083 (031896-042000)			
; CURRENT APPLICATION NUMBER: US/11/060,756			
; CURRENT FILING DATE: 2005-02-18			
; NUMBER OF SEQ ID NOS: 303284			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 2817			
; LENGTH: 600			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-11-060-756-2817			
Query Match 47.6%; Score 600; DB 10; Length 600;			
Best Local Similarity 100.0%; Pred. No. 6.5e-176;			
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	662	GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCATCTCTGAAACGACTCTG	721
Db	1	GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCATCTCTGAAACGACTCTG	60
Qy	722	GCCTCTACACCTGCAATGTGTCCGGGAGTTTGAGTTTGGGGCGCATCGGCCCTTTGTGA	781
Db	61	GCCTCTACACCTGCAATGTGTCCGGGAGTTTGAGTTTGGGGCGCATCGGCCCTTTGTGA	120
Qy	782	AGACGACGGCGGTGATCCCCCTTAAGAGTCAACCGAGGAGGCTGGAGAGGACTTCACCTCTG	841
Db	121	AGACGACGGCGGTGATCCCCCTTAAGAGTCAACCGAGGAGGCTGGAGAGGACTTCACCTCTG	180
Qy	842	TGGFTCTCAGAAATCATGATGATGATGATCATCTTCTGGFTTTCCTCAACCCCTGTGGCTGCTCATCG	901

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RESULT 4
US-11-060-756-2817
; Sequence 2817, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles o
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2817
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2817

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	Query Match	47.6%	Score 600	DB 10	Length 600	
	Best Local Similarity	100.0%	Pred. No. 6.5e-176			
	Matches 600	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	662	GCAGCAGGACCTGCAGGAGCTGCCATCACTGTGCTCAACGTCACCTCTCAACGACACTCTG	721			
Db	1	GCAGCAGGACCTGCAGGAGCTGCCATCACTGTGCTCAACGTCACCTCTGACGACACTCTG	60			
QY	722	GCCTCTACCTGCAATGTCTCCGGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGA	781			
Db	61	GCCTCTACCTGCAATGTCTCCGGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGA	120			
QY	782	AGACGACGGCGCTGATCCCCCTAAGAGTCAACGAGGAGGCTTGAGAGGACTTCACCTCTG	841			
Db	121	AGACGACGGCGCTGATCCCCCTAAGAGTCAACGAGGAGGCTTGAGAGGACTTCACCTCTG	180			
QY	842	TGCTCTCAGAAATCATGATGATCATCTCTGGTCTTCCTCACCCCTGTGCTGCTCATCG	901			

Db 181 TGGTCTCAGAAATCATGATGTACATCTCTCTGGTCTTCTCCCTCACCTGTGGTGTCTCATCG 240
Qy 902 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGGT 961
Db 241 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGGT 300
Qy 962 CTGACTACTTGGCCATCCCATCTCAGAACAAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 1021
Db 301 CTGACTACTTGGCCATCCCATCTCAGAACAAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 360
Qy 1022 AGAACAGGAGCAGTGTGACATGAGGTGGCTTGAACACCTGAGGAGCTGGACATCCCATGT 1081
Db 361 AGAACAGGAGCAGTGTGACATGAGGTGGCTTGAACACCTGAGGAGCTGGACATCCCATGT 420
Qy 1082 TCAGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCCCATCGCTTCCCTTCATGCA 1141
Db 421 TCAGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCCCATCGCTTCCCTTCATGCA 480
Qy 1142 TCCATTGTTCTGTTCAATTCATTCATCCATACATCCACCTGCTCTGAGCTTTCACCTCTG 1201
Db 481 TCCATTGTTCTGTTCAATTCATTCATCCATACATCCACCTGCTCTGAGCTTTCACCTCTG 540
Qy 1202 ACTCCCTAACTCCATCAGACCTCTACGCCACCATAGACTCTGCCAGAACTGAGAAGCGGG 1261
Db 541 ACTCCCTAACTCCATCAGACCTCTACGCCACCATAGACTCTGCCAGAACTGAGAAGCGGG 600

RESULT 5
US-11-060-756-7088
; Sequence 7088, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7088
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7088

Query Match 47.6%; Score 600; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 6.5e-176;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 662 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTG 721
Db 1 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTG 60
Qy 722 GCCTCTACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGA 781
Db 61 GCCTCTACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGA 120
Qy 782 AGACGACGGCTGTATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTTCACCTCTG 841
Db 121 AGACGACGGCTGTATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTTCACCTCTG 180
Qy 842 TGGTCTCAGAAATCATGATGTACATCCTTCTGGTCTTCTCACCCTGTGGCTGTCTCATCG 901
Db 181 TGGTCTCAGAAATCATGATGTACATCCTTCTGGTCTTCTCACCCTGTGGCTGTCTCATCG 240
Qy 902 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGGT 961
Db 241 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGGT 300
Qy 962 CTGACTACTTGGCCATCCCATCTGAGAACAAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 1021

Db 301 CTGACTACTTGGCCATCCCATCTCAGAACAAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 360
Qy 1022 AGAACAGGAGCAGTGTGACATGAGGTGGCTTGAACACCTGAGGAGCTGGACATCCCATGT 1081
Db 361 AGAACAGGAGCAGTGTGACATGAGGTGGCTTGAACACCTGAGGAGCTGGACATCCCATGT 420
Qy 1082 TCAGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCCCATCGCTTCCCTTCATGCA 1141
Db 421 TCAGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCCCATCGCTTCCCTTCATGCA 480
Qy 1142 TCCATTGTTCTGTTCAATTCATTCATCCATACATCCACCTGCTCTGAGCTTTCACCTCTG 1201
Db 481 TCCATTGTTCTGTTCAATTCATTCATCCATACATCCACCTGCTCTGAGCTTTCACCTCTG 540
Qy 1202 ACTCCCTAACTCCATCAGACCTCTACGCCACCATAGACTCTGCCAGAACTGAGAAGCGGG 1261
Db 541 ACTCCCTAACTCCATCAGACCTCTACGCCACCATAGACTCTGCCAGAACTGAGAAGCGGG 600

RESULT 6
US-11-060-756-7089
; Sequence 7089, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7089
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7089

Query Match 47.6%; Score 600; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 6.5e-176;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 662 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTG 721
Db 1 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTG 60
Qy 722 GCCTCTACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGA 781
Db 61 GCCTCTACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGA 120
Qy 782 AGACGACGGCTGTATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTTCACCTCTG 841
Db 121 AGACGACGGCTGTATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTTCACCTCTG 180
Qy 842 TGGTCTCAGAAATCATGATGTACATCCTTCTGGTCTTCTCACCCTGTGGCTGTCTCATCG 901
Db 181 TGGTCTCAGAAATCATGATGTACATCCTTCTGGTCTTCTCACCCTGTGGCTGTCTCATCG 240
Qy 902 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGGT 961
Db 241 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGGT 300
Qy 962 CTGACTACTTGGCCATCCCATCTGAGAACAAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 1021
Db 301 CTGACTACTTGGCCATCCCATCTGAGAACAAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 360
Qy 1022 AGAACAGGAGCAGTGTGACATGAGGTGGCTTGAACACCTGAGGAGCTGGACATCCCATGT 1081
Db 361 AGAACAGGAGCAGTGTGACATGAGGTGGCTTGAACACCTGAGGAGCTGGACATCCCATGT 420
Qy 1082 TCAGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCCCATCGCTTCCCTTCATGCA 1141

Db 493 GACTGATACCTTTGCGAGTCACTGAAGAGCGGAGAAAGACTTCACTCCGTGCTCGG 552
Qy 851 AAATCATGATGATACATCTTCTGGTCTCTCCACACCTGTGCTGCTCATCGAGATGATAT 910
Db 553 AAATCATGATGATACATCTTCTGGTCTCTCCACCTTGTGGCTGCTTTATTGAGATGATCT 612
Qy 911 ATTGCTACAGAAAGGTCTCAAAAGCCGAAGAGGAGCGCCCAAGAAACGCGTCTCACTACC 970
Db 613 ATTGCTACAGAAAGGTCTCTAAGGCCGAAGAGGAGGACACAGAAATGCGTCTCACTACC 672
Qy 971 TTGGCATCCCATCTGAGAACAGGAGAACTCTGGGTACCACTGAGGAGTGGAGAAATAGAACAGGA 1030
Db 673 TTGCTATCCCTTCAGAGAACAGGAGAACTCTGTGGTACCTGTGGAGAAATA-----AT 726
Qy 1031 GCAGTGTGACATGAGGTGGCTGAAACACCTGAGGAGCTGGACATCCCATGTTTCAGCAATG 1090
Db 727 GTGGTGTGACTTGAGGTGATCTG-AGTGTGAGGAGCTGGATATCCCCAGTTTCAGTGTATG 785
Qy 1091 TCAATGGCATCAGAGGGCGCCCAAGGGCCCCATCGCTTCCCTTCATGCAATCCAT 1146
Db 786 CCAGCAATATCAGGAAGTGCCCAAGGTGTGCCCAACACATCCATCTTTTCTATTTCAT 841

RESULT 9

US-10-029-191-1
; Sequence 1, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A. J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3108
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-1

Query Match 44.4%; Score 559.6; DB 5; Length 3108;
Best Local Similarity 84.4%; Pred. No. 4.5e-163;
Matches 655; Conservative 0; Mismatches 114; Indels 7; Gaps 2;
Qy 371 AGAAGATCGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATCTACTGGG 430
Db 73 AAAAGATCGCTGCTTCAACAGATTGCTTCCCTAGCTTCTTAGTGTCTACTACTGGG 132
Qy 431 TCAGTGTCTGCTTCCCTGTGTGTGGAGTGGTCCCTCGAGACGAGGCGCTGACGGCA 490
Db 133 TCAGAGTCTGCTTCCCTGTGTGTGGAGTGGTCCCTCGAGACAGAAAGCGGTGACGGCA 192
Qy 491 ACCCATGAAGTGGCTGCATCTCTCGATGAAGAGAGAGGTGGAGGCCACACCGG 550
Db 193 ATCCCATGAAGTGAAGTGCATCTCTCGATGAAGAGAGAGGTGGAGGCCACCATG 252
Qy 551 TGGTGGAAATGGTTTACAGGCCCGAGGCGGTAAGATTCTTATTATTACAGTATCGGA 610
Db 253 TGGTGGAGTGGTTTACAGGCCCTGAGGCGGTAAGATTCTTATATATAGTATCGGA 312
Qy 611 ATGGCCACAGAGGTGGAGAGCCCTTTCAGGGCGGCTGAGTGGAAATGGCAGCAAGG 670
Db 313 ATGGCCACAGGAAGTGGAGAGCCCTTTCAGAGGCCGTGTCAGTGGAAATGGAGCAAG 372
Qy 671 ACCTGAGAGCGTGTCCATCACTGTGCTCAAGCTCACTGTGAACGACTCTGGCTCTTACA 730

Db 373 ACCTGAGGAGCGTATCCATCACTGTACTCAATGTCACTTTGAATGATCTGGGCTCTACA 432
Qy 731 CCTGCAATGTGTCGCGGAGTTTGTAGTTTGTAGGCGCATCGCCCTTTGTGAAGACGACGC 790
Db 433 CATGCAATGTGTCAGGAGTTTGAATTCGAGGACACAGGCCCTTTTGTGAAGACGACGA 492
Qy 791 GGCTGATCCCCCTTAAGAGTCAACGAGGAGGTCTGGAGAGGACTTCACCTCTGTGTCTCAG 850
Db 493 GACTGATACCTTTTCCGAGTCACTGAAGAGCGGAGAGAACTTCACCTCCGTGCTCGG 552
Qy 851 AAATCATGATGATACATCTTCTGGTCTTCTCACCCTGTGGCTGCTCATCGAGATGATAT 910
Db 553 AAATCATGATGATACATCTTCTGGTCTTCTCACCCTGTGGCTGCTTTTATTGAGATGATCT 612
Qy 911 ATTGCTACAGAAAGGTCTCAAAAGCCGAAGAGGAGCGCCCAAGAAACGCGTCTCACTACC 970
Db 613 ATTGCTACAGAAAGGTCTCTAAGGCCGAAGAGGAGGACACAGAAATGCGTCTCACTACC 672
Qy 971 TTGGCATCCCATCTGAGAACAGGAGAACTCTGGGTACCACTGAGTGGAGAAATAGAACAGGA 1030
Db 673 TTGCTATCCCTTCAGAGAACAGGAGAACTCTGTGGTACCTGTGGAGAAATA-----AT 726
Qy 1031 GCAGTGTGACATGAGGTGGCTGAAACACCTGAGGAGCTGGACATCCCATGTTTCAGCAATG 1090
Db 727 GTGGTGTGACTTGAGGTGATCTG-AGTGTGAGGAGCTGGATATCCCCAGTTTCAGTGTATG 785
Qy 1091 TCAATGGCATCAGAGGGCGCCCAAGGGCCCCATCGCTTCCCTTCATGCAATCCAT 1146
Db 786 CCAGCAATATCAGGAAGTGCCCAAGGTGTGCCCAACACATCCATCTTTTCTATTTCAT 841

RESULT 10

US-09-977-579-3
; Sequence 3, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
; TITLE OF INVENTION: channel
; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977,579
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: rat
US-09-977-579-3

Query Match 42.8%; Score 540; DB 3; Length 2220;
Best Local Similarity 89.3%; Pred. No. 5.1e-157;
Matches 582; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
Qy 371 AGAAGATCGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATCTACTGGG 430
Db 358 AAAAGATCGCTGCTTCAACAGATTGCTTCCCTAGCTTCTTAGTGTCTACTACTGGG 417
Qy 431 TCAGTGTCTGCTTCCCTGTGTGTGGAGTGGTCCCTCGAGACGAGGCGCTGACGGCA 490
Db 418 TCAGAGTCTGCTTCCCTGTGTGTGGAGTGGTCCCTCGAGACAGAAAGCGGTGACGGCA 477
Qy 491 ACCCATGAAGTGGCTGCAATCTCTCGATGAAGAGAGAGGTGGAGGCCACACCGG 550
Db 478 ATCCCATGAAGTGGAGTGGCAATCTCTCGATGAAGAGGAGAGGTGGAGGCCACCATG 537
Qy 551 TGGTGGAAATGGTTTACAGGCCCGAGGCGGTAAGATTCTTATTATTACAGTATCGGA 610

Db 538 TGGTGGAGTGGTCTACAGGCGCTGAGGCGGTAAAGATTTCTTATATATAGTATCGGA 597
Qy 611 ATGGCCACCGAGAGTGGAGAGCCCTTTTCAGGGCGCTCGAGTGGGAATGGCAGCAAG 670
Db 598 ATGGCCACCGAGAGTGGAGAGCCCTTTTCAGGGCGCTCGAGTGGGAATGGGAGCAAG 657
Qy 671 ACCTGCAGGAGTGCATCATCTGCTCAAGTCACTCTGAAGACTCTGGCTCTTACA 730
Db 658 ACCTGCAGGAGTATCCATCATCTGCTCAATGTCACTTTGAATGACTCTGGCTCTTACA 717
Qy 731 CCTGCAATGTCTCCGGAGTGTGAGTTGAGGGCGCATCGGCCCTTTGTGAAGACGAGCG 790
Db 718 CATGCAATGTCTCAGGAGTTCGAATTCGAGGCACACAGGCCCTTTGTGAAGACGAGCG 777
Qy 791 GGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGGAGCTTCACTCTGTGTCTCAG 850
Db 778 GACTGATACCTTTGCGAGTCACTGAAGAGGCGGAGAGACTTCACTCTCGGTCTCGG 837
Qy 851 AAATCATGATGATACCTCTCTGCTCTTCCCTCACCCTGTGCTGCTCATCGAGATGAT 910
Db 838 AAATCATGATGATACCTCTCTGCTCTTCCCTCACCCTGTGCTGCTGTTATTGAGATGAT 897
Qy 911 ATTGCTACAGAAAGTCTCAAAAGCCGAAGAGGCGCCCAAGAAACGCGTCTCACTACC 970
Db 898 ATTGCTACAGAAAGTCTCAAGGCCGAAGAGGCGACACAGAAATGCGTCTGACTACC 957
Qy 971 TTGCTATCCCTTCAGAGAAAGGAGAACTCTGTGGTACCTGTGGAGGAATA 1022
Db 958 TTGCTATCCCTTCAGAGAAAGGAGAACTCTGTGGTACCTGTGGAGGAATA 1009

RESULT 11

US-10-029-191-21
; Sequence 21, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 21
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-21

Query Match 42.4%; Score 534.6; DB 5; Length 645;
Best Local Similarity 89.3%; Pred. No. 1.6e-155;
Matches 576; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 376 ATGCTGCTCAATAGATTGTTCCCTGCTGCTTCTCTGCTGCTTACTGCTGCTAGT 435
Db 1 ATGCTGCTCAACAGATTGCTTCCCTGCTGCTTCTCTGCTGCTTACTGCTGCTAGT 60
Qy 436 GTCTGCTTCCCTGTGTGTGGAAGTGCCTCGAGAGCGAGGCGGTGAGGCGCAACCC 495
Db 61 GTCTGCTTCCCTGTGTGTGGAAGTGCCTCGAGAGCGAGGCGGTGAGGCGCAATCCC 120
Qy 496 ATGAAGCTGCTGCTGCTCTCTGATGAAGAGAGAGGAGTGGAGGCGCACCAACCGTGGT 555
Db 121 ATGAAGCTGCTGCTGCTCTCTGATGAAGAGAGAGGAGTGGAGGCGCACCAACCGTGGT 180
Qy 556 GAATGGTCTACAGGCGCGGCGGTAAAGATTTCTTATTACGAGTATCGGAATGGC 615
Db 181 GAGTGGTCTACAGGCGCGGCGGTAAAGATTTCTTATTATGATATCGGAATGGC 240

Qy 616 CACCAGAGTGGAGAGCCCTTTTCAGGGCGCTCGAGTGGGAATGGCAGCAAGACCTG 675
Db 241 CACCAGAGTGGAGAGCCCTTTTCAGGGCGCTCGAGTGGGAATGGGAGCAAGACCTG 300
Qy 676 CAGGAGCTGCTCACTGCTCAAGTCACTCTGAAGACTCTGGGCTCTTACACCTGC 735
Db 301 CAGGAGCTGCTCACTGCTCAATGTCACTTTGAATGACTCTGGGCTCTTACACATGC 360
Qy 736 AATGTGCTCCGGAGTGTGAGTTGAGGCGCATCGGCCCTTTGTGAAGACGAGCGGCTG 795
Db 361 AATGTGCTCCGGAGTGTGAGTTGAGGCGCATCGGCCCTTTGTGAAGACGAGCGCTG 420
Qy 796 ATCCCTTAAAGTCAACGAGGAGGCTGGAGAGCTTCACTCTGTGTGCTTACAGAAATC 855
Db 421 ATACCTTTGGAGTCACTGAAGAGGCGGAGAGACTTCACTCTCGTGGTCTCGGAATC 480
Qy 856 ATGATGTACATCTCTGCTCTTCCCTCACCCTGTGCTGCTCATCGAGATGATATATGC 915
Db 481 ATGATGTACATCTCTGCTCTTCCCTCACCCTGTGCTGCTTATTTGAGATGATCTATTC 540
Qy 916 TACAGAAAGTCTCAAAAGCGGAGAGGCGCCCAAGAAACGCGTCTGACTACCTTCCC 975
Db 541 TACAGAAAGTCTCTAAGGCCGAAGAGGCGACAGGAAATGCGTCTGACTACCTTGGT 600
Qy 976 ATCCATCTGAGAAACAGGAGAACTCTGCGGTACCACTGAGTGGAGGAA 1020
Db 601 ATCCCTTCAGAGAAACAGGAGAACTCTGTGGTACCTGTGGAGGAA 645

RESULT 12

US-09-925-065A-513769
; Sequence 513769, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957085
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513769
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-513769

Query Match 33.0%; Score 416; DB 4; Length 651;
Best Local Similarity 99.8%; Pred. No. 1.4e-118;
Matches 427; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 3 CTCCTTCCGAGCTGAGCTTACCTGGCGCAACAGCAGCGAGCGGCGCGAGTGGAA 62
Db 131 CTCCTTCCGAGCTGAGCTTACCTGGCGCAACAGCAGCGAGCGGCGCGAGTGGAA 189
Qy 63 GCTGAGTTCGGGGTGGGGGAGGCGAGCTGCTCGTGTGTGCTGAGCGCGGCGAGC 122
Db 190 GCTGAGTTCGGGGTGGGGGAGGCGAGCTGCTCGTGTGTGCTGAGCGCGGCGAGC 249
Qy 123 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGCTCCAGTGGGCTCGCTAGG 182

Db 250 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGTCGCTTAGGG 309
Qy 183 CCAAAGCCCCACCGGCTCCAAAGCTCCAGGGCTCCCAAGGACCGGTGCTCGGC 242
Db 310 CCAAAGCCCCACCGGCTCCAAAGCTCCAGGGCTCCCAAGGACCGGTGCTCGGC 369
Qy 243 CTTCTCTTCGGTCAAGAGTCCGCCCTGGGGGAGTTCGTCCTCAAGAGGTTTCTCGAA 302
Db 370 CTTCTCTTCGGTCAAGAGTCCGCCCTGGGGGAGTTCGTCCTCAAGAGGTTTCTCGAA 429
Qy 303 AGAATCTGAGAGGCGCAGTCTTTGACCGAGGGAATCTCTGTGTAGCCCTTGAAGCCG 362
Db 430 AGAATCTGAGAGGCGCAGTCTTTGACCGAGGGAATCTCTGTGTAGCCCTTGAAGCCG 489
Qy 363 CCAGCCCCAGAGATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTAT 422
Db 490 CCAGCCCCAGAGATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTAT 549
Qy 423 CTACTGGG 430
Db 550 CTACTGGG 557

RESULT 13

US-09-925-065A-513767
; Sequence 513767, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513767
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-513767

Query Match 33.0%; Score 415.6; DB 4; Length 651;
Best Local Similarity 99.5%; Pred. No. 1.8e-118;
Matches 426; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Qy 3 CTCCTTCGAGCTGAGCTTACCTTGGGGGCAAGCAGGAGCGAGGGCGGAGTGAA 62
Db 131 CTCCTTCGAGCTGAGCTTACCTTGGGGGCAAGCAGGAGCGAGTGAA 189
Qy 63 GCTGGAGTTCGGGGTGGGGGAGGAGTCTCGGTGCTGAGCGCGGCGAGAGC 122
Db 190 GCTGGAGTTCGGGGTGGGGGAGGAGTCTCGGTGCTGAGCGCGGCGAGAGC 249
Qy 123 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTTCGCTTAGGG 182
Db 250 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTTCGCTTAGGG 309
Qy 183 CCAAAGCCCCACCGGCTCCAAAGCTCCAGGGCTCCCAAGGACCGGTGCTCGGC 242
Db 310 CCAAAGCCCCACCGGCTCCAAAGCTCCAGGGCTCCCAAGGACCGGTGCTCGGC 369
Qy 243 CTTCTCTTCGGTCAAGAGTCCGCCCTGGGGGAGTTCGTCCTCAAGAGGTTTCTCGAA 302

Db 370 CTTCTCTTCGGTCAAGAGTCCGCCCTGGGGGAGTTCGTCCTCAAGAGGTTTCTCGAA 429
Qy 303 AGAATCTGAGAGGCGCAGTCTTTGACCGAGGGAATCTCTGTGTAGCCCTTGAAGCCG 362
Db 430 AGAATCTGAGAGGCGCAGTCTTTGACCGAGGGAATCTCTGTGTAGCCCTTGAAGCCG 489
Qy 363 CCAGCCCCAGAGATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTAT 422
Db 490 CCAGCCCCAGAGATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTAT 549
Qy 423 CTACTGGG 430
Db 550 CTACTGGG 557

RESULT 14

US-09-925-065A-513768
; Sequence 513768, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513768
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-513768

Query Match 33.0%; Score 415.6; DB 4; Length 651;
Best Local Similarity 99.5%; Pred. No. 1.8e-118;
Matches 426; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Qy 3 CTCCTTCGAGCTGAGCTTACCTTGGGGGCAAGCAGGAGCGAGGGCGGAGTGAA 62
Db 131 CTCCTTCGAGCTGAGCTTACCTTGGGGGCAAGCAGGAGCGAGTGAA 189
Qy 63 GCTGGAGTTCGGGGTGGGGGAGGAGCAGTCTCGGTGCTGAGCGCGGCGAGAGC 122
Db 190 GCTGGAGTTCGGGGTGGGGGAGGAGCAGTCTCGGTGCTGAGCGCGGCGAGAGC 249
Qy 123 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTTCGCTTAGGG 182
Db 250 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTTCGCTTAGGG 309
Qy 183 CCCAAAGCCCCACCGGCTCCAAAGCTCCAGGGCTCCCAAGGACCGGTGCTCGGC 242
Db 310 CCCAAAGCCCCACCGGCTCCAAAGCTCCAGGGCTCCCAAGGACCGGTGCTCGGC 369
Qy 243 CTTCTCTTCGGTCAAGAGTCCGCCCTGGGGGAGTTCGTCCTCAAGAGGTTTCTCGAA 302
Db 370 CTTCTCTTCGGTCAAGAGTCCGCCCTGGGGGAGTTCGTCCTCAAGAGGTTTCTCGAA 429
Qy 303 AGAATCTGAGAGGCGCAGTCTTTGACCGAGGGAATCTCTGTGTAGCCCTTGAAGCCG 362
Db 430 AGAATCTGAGAGGCGCAGTCTTTGACCGAGGGAATCTCTGTGTAGCCCTTGAAGCCG 489

Job time : 1444 secs

Qy 363 CCAGCCCAAGAGATGCTGCTTCAATAGATTGTTTCCCTGCGCTTCTCTCGTGTAT 422
Db 490 CCAGCCCAAGAGATGCTGCTTCAATAGATTGTTTCCCTGCGCTTCTCTCGTGTAT 549
Qy 423 CTAAGGG 430
Db 550 CTAAGGG 557

RESULT 15
US-10-450-763-22567
; Sequence 22567, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22567
; LENGTH: 3531
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (300)..(407)
; OTHER INFORMATION: 94% homologous to Homo sapiens putative kruppel-related zinc
; OTHER INFORMATION: finger protein NY-REN-23 antigen, accession number AF155101, Smith-
; OTHER INFORMATION: Waterman Score=180.
US-10-450-763-22567

Query Match 31.1%; Score 392.6; DB 9; Length 3531;
Best Local Similarity 99.0%; Pred. No. 4.8e-111;
Matches 395; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 422 TCTACTGGTCAGTGTCTGCTTCCCTGTGTGTGGAAGTCCCTCGGAGACGGAGCGCG 481
Db 2951 TCAGGTGTGTCTGCTTCCCTGTGTGTGGAAGTCCCTCGGAGACGGAGCGCG 3010
Qy 482 TGCAGGGCAACCCCATGAAGCTGCGTGCATCTCTGATGAAGAGAGAGAGTGGAGG 541
Db 3011 TGCAGGGCAACCCCATGAAGCTGCGTGCATCTCTGATGAAGAGAGAGAGTGGAGG 3070
Qy 542 CCACACGGTGGTGAATGGTTCTACAGGCCGAGGGCGGTAAAGATTTCCTTATTTACG 601
Db 3071 CCACACGGTGGTGAATGGTTCTACAGGCCGAGGGCGGTAAAGATTTCCTTATTTACG 3130
Qy 602 AGTATCGGAATGGCCACAGAGGTGGAGAGCCCTTTTCAGGGCGCGCTCGAGTGAATG 661
Db 3131 AGTATCGGAATGGCCACAGAGGTGGAGAGCCCTTTTCAGGGCGCGCTCGAGTGAATG 3190
Qy 662 GCAGCAAGGACCTCGAGAGCGTGTCCATCACTGTCTCAAGTCACTCTGAACGACTCTG 721
Db 3191 GCAGCAAGGACCTCGAGAGCGTGTCCATCACTGTCTCAAGTCACTCTGAACGACTCTG 3250
Qy 722 GCCTCTACCTGCAATGTGTCCGGGAGTTTGAAGTTTGAGGGCGCATCGGCCCTTTGTGA 781
Db 3251 GCCTCTACCTGCAATGTGTCCGGGAGTTTGAAGTTTGAGGGCGCATCGGCCCTTTGTGA 3310
Qy 782 AGACGACGGGCTGATCCCCCTAAGAGTCAACCGAGGAGG 820
Db 3311 AGACGACGGGCTGATCCCCCTAAGAGTCAACCGAGGAGG 3349

Search completed: December 13, 2005, 14:31:24

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Qy 241 GCCCTCTCCGCTCAGAAAGTCGCCCTCGGGGGCAGTTGCTCCCAAGGGTTTCCTCG 300
Db |||||
Qy 241 GCCCTCTCCGCTCAGAAAGTCGCCCTCGGGGGCAGTTGCTCCCAAGGGTTTCCTCG 300
Db |||||
Qy 301 AAAGAATCTGAGAGGGCGCAGTCTCTGACCGAGGAATCTCTCTGTGTAGCCTTTGGAAGC 360
Db |||||
Qy 301 AAAGAATCTGAGAGGGCGCAGTCTCTGACCGAGGAATCTCTCTGTGTAGCCTTTGGAAGC 360
Db |||||
Qy 361 CGCAGAGCCCAAGATGCTCGCTTCAATAGATTGTTCCCTCGGCTTCTCTCGTCTT 420
Db |||||
Qy 361 CGCAGAGCCCAAGATGCTCGCTTCAATAGATTGTTCCCTCGGCTTCTCTCGTCTT 420
Db |||||
Qy 421 ATCTACTGGGTGCTGCTGCTCCCTGTGTGTGGAAGTGCCTCGGAGCGAGGCC 480
Db |||||
Qy 421 ATCTACTGGGTGCTGCTGCTCCCTGTGTGTGGAAGTGCCTCGGAGCGAGGCC 480
Db |||||
Qy 481 GTGCAAGGCCAACCCATGAAGCTCGCTGTCATCTCTGCAATGAAGAGAGAGGAGGTGGAG 540
Db |||||
Qy 541 GCCACCAAGTGTGGATGTTCTACAGGCCCGAGGCGGTAAAGATTTCCTTTATTAC 600
Db |||||
Qy 541 GCCACCAAGTGTGGATGTTCTACAGGCCCGAGGCGGTAAAGATTTCCTTTATTAC 600
Db |||||
Qy 601 GAGTATCGGAATGCCACAGAGGTGGAGAGCCCTTTTCAGGGGCGCTGCACTGGAAT 660
Db |||||
Qy 601 GAGTATCGGAATGCCACAGAGGTGGAGAGCCCTTTTCAGGGGCGCTGCACTGGAAT 660
Db |||||
Qy 661 GGCAAGCAAGCACTGCAAGAGCTGTCATCACTGTGCTCAACGTCACCTGTAACGACTCT 720
Db |||||
Qy 661 GGCAAGCAAGCACTGCAAGAGCTGTCATCACTGTGCTCAACGTCACCTGTAACGACTCT 720
Db |||||
Qy 721 GGCCTCTACACTGCAATGTGTCCGGAGTTTGAGTTGAGGGCGATCGGCCCTTTGTG 780
Db |||||
Qy 721 GGCCTCTACACTGCAATGTGTCCGGAGTTTGAGTTGAGGGCGATCGGCCCTTTGTG 780
Db |||||
Qy 781 AAGACGAGCGGCTGATCCCTTAAGAGTCAACGAGAGGCTGAGAGGACTTCACCTCT 840
Db |||||
Qy 781 AAGACGAGCGGCTGATCCCTTAAGAGTCAACGAGAGGCTGAGAGGACTTCACCTCT 840
Db |||||
Qy 841 GTGCTCTCAGAAATCATGATGATCATCTCTGCTGCTTCTCCTCACCTCTGCTCATC 900
Db |||||
Qy 841 GTGCTCTCAGAAATCATGATGATCATCTCTGCTGCTTCTCCTCACCTCTGCTCATC 900
Db |||||
Qy 901 GAGATGATATATGCTACAGAAAGGTCTCAAAAGCCGAGAGGCGCAAGAAAACGG 960
Db |||||
Qy 901 GAGATGATATATGCTACAGAAAGGTCTCAAAAGCCGAGAGGCGCAAGAAAACGG 960
Db |||||
Qy 961 TCTGACTACCTTGCCATCCCATCTGAGAAACAGAGAACTCTGCGGTACCACTGAGGAA 1020
Db |||||
Qy 961 TCTGACTACCTTGCCATCCCATCTGAGAAACAGAGAACTCTGCGGTACCACTGAGGAA 1020
Db |||||
Qy 1021 TAGAACAGGACAGTGTGACATGAGGTGGCTGAAACACCTGAGGAGCTGGAATCCCATG 1080
Db |||||
Qy 1021 TAGAACAGGACAGTGTGACATGAGGTGGCTGAAACACCTGAGGAGCTGGAATCCCATG 1080
Db |||||
Qy 1081 TTGAGCAATGCAATGGCATCAGAGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGC 1140
Db |||||
Qy 1081 TTGAGCAATGCAATGGCATCAGAGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGC 1140
Db |||||
Qy 1141 ATCCATTGTTCTGTTTCATTTCATTCATCATATCCACCTGCTGAGCTTTTCACCTCT 1200
Db |||||
Qy 1141 ATCCATTGTTCTGTTTCATTTCATTCATCATATCCACCTGCTGAGCTTTTCACCTCT 1200
Db |||||
Qy 1201 GACTCCCTTAACTCCATCAGACTCTTACGCACCATTAAGACTCTGCGCAGAACTGAGAAGCG 1260
Db |||||
Qy 1201 GACTCCCTTAACTCCATCAGACTCTTACGCACCATTAAGACTCTGCGCAGAACTGAGAAGCG 1260
Db |||||
Qy 1261 G 1261
Db 1261 G 1261

RESULT 2
US-10-374-954-4
; Sequence 4, Application US/10374954
; Publication No. US2005026057eA1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(681)
US-10-374-954-4

Query Match 11.4%; Score 143.8; DB 6; Length 1335;
Best Local Similarity 56.9%; Pred. No. 1.3e-30;
Matches 334; Conservative 0; Mismatches 232; Indels 21; Gaps 3;

Qy 441 CTTCCCTGTGTGTGGAAAGTGCCTCGAGAGCGGAGCGGTGCGAGGCAACCCCATGAA 500
Db 75 TCGGGGGGTGCGTGAGGTGAGCTCGAGACGAGCGCGGTATGGGTGACTTCAA 134
Qy 501 GCTGCGCTGCTATCTCTGCATGAAGAGAGAGGAGGTGGAGGCCACCGGTGGGAATG 560
Db 135 AATTCTTTGCTATCTCTGCAAGCGCCGAGCGACCAACGCTGAGACCTTCACCGAGTG 194
Qy 561 GTTCTACAGCGCGGCGGTAAAGATT-----TCCTTATTTACGAGTATCGAA 611
Db 195 GACCTTCGCGCAGAAAGGCGCATGAGGAGTTTGTCAAGATCCTGCGCTATGAGAATGAGGT 254
Qy 612 TGGCCACAGAGGTGAGAGCGCTTTTCAGGGGCGCTGCGAGTGGGAATGGCAG----- 665
Db 255 GTTCAGCTGAGAGAGGTGAGCGCTTCGAGGGCGCGTGGTGTGGAAATGGCAGCGGG 314
Qy 666 ---CAAGGACCTGCAAGACGTTGTCATCACTGTGCTCAACGTCACTCTGAAACGACTCTGG 722
Db 315 CACCAAGACCTGCAAGACGTTGTCATCACTCAACAAATGTCACCTACCAACCACTCGGG 374
Qy 723 CTTCTACACCTGCAATGTTCCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAA 782
Db 375 CGACTACAGTGCACCGCTTACCGCCTGCTCTTCGAAACTACGAGCAACACCGAG 434
Qy 783 GACGACGCGCTGATCCCTCTAAGAGTCAACGAGAGGCTGGAGAGGACTTCACCTCTGT 842
Db 435 CGTCTCAAGAGATCACATTTAGGTAGTGGACAAAGCCAAACAGAGACATGGCATCCAT 494
Qy 843 GGTCTCAGAAATCATGATGATCATCTCTGTGTTCTTCTCAACCTGTGGTGTGCTCATGA 902
Db 495 CGTGTCTGAGATCATGATGATGCTCATTTGTTGTTGACCATATATGGCTTCGTGGCAGA 554
Qy 903 GATGATATATGCTACAGAAAGGTCTCAAAAGCCGAAAG---CGACCCCAAGAAAACGC 959
Db 555 GATGATTTACTGCTACAGAAAGATCGGTGCGCCACCGAGACTGCTGACAGGAGAAATGC 614
Qy 960 GTCTGACTTACCTTGCCTATCCATCTGAGAAACAGAGAACTCTCTGCGG 1006
Db 615 CTGGAATACCTGGCCATCACCTCTGAAAGCAAGAGAACTGCACGG 661

RESULT 3
US-10-750-185-44336


```
; LENGTH: 193789
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-55

Query Match          4.0%; Score 51; DB 7; Length 193789;
Best Local Similarity 58.1%; Pred. No. 0.00072;
Matches 90; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 441 CTTCCCTGTGTGTGGAGTGCCTCGAGACGGAGCGCGTGCAGGCAACCCCATGAA 500
Db 102787 CTGGGGGGCTGCGTGGAGGTGGACTCGGAGACCGAGGCGGTGTATGGATGACCTTCAA 102846

Qy 501 GCTCGCTGTCATCTCTCATGAAGAGAGAGAGGTGGAGGCCACCAACGGTGGTGGGAATG 560
Db 102847 AATCTTTGCAATCTCTCAAGCGCGCGAGGAGACCAACCTGAGACCTTACCGAGTG 102906

Qy 561 GTTCTACAGGCCGAGGCGGTAAAGATTTCTTTA 595
Db 102907 GACCTTCGCCAGAGGGCACTGAGGAGTTTGTC A 102941

RESULT 7
US-11-121-086-61/c
; Sequence 61, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: FOULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 169495
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (70072)..(70171)
; OTHER INFORMATION: a, c, g, t, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (139457)..(157244)
; OTHER INFORMATION: a, c, g, t, unknown or other
US-11-121-086-61

Query Match          3.6%; Score 44.8; DB 7; Length 169495;
Best Local Similarity 56.7%; Pred. No. 0.037;
Matches 102; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

Qy 74 GGGGTGGCGGGAGCGCACTGTCGTGCTGAGCGCCGCGAGAGCGGCGCGAGC 133
Db 45491 GGGAGGGCGGTAGGGACCTTTTCAGAGCAGAGGGGCTTTCCGGGGCGGTGGGGCGCGC 45432

Qy 134 GCGTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTCG-CTTAGGGGCCAAAGCCC 192
Db 45431 TCGGAGCGGAGCGCGGCTCGACGCGGTGCGCTGGCGGCGAGTGTATGACAGCGGCGC 45372

Qy 193 CCACCGGCTCAAAAAGTCCACAGGCGCTCCACAGGCAACCGGTGCTGGCCCTTCTTCG 252
Db 45371 CGGGCCCGAACCAGCCGAGCCCGCGGGGCTCCCAACCGCGGCTTCCCGCCCTCCCGCG 45312

RESULT 8
US-10-770-726-27
; Sequence 27, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-27

Query Match          3.2%; Score 40.2; DB 6; Length 2838;
Best Local Similarity 49.8%; Pred. No. 0.14;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Qy 23 ACCTGGGCGCAACAGCAGCGAGCGGGCGCGAGTGGAGCTTCCGGGGTGGC 82
Db 577 ACCACGCCAGAGGGGCCCCAGGAGGAGGAGCGCGGTTCCGCCGTACAGC 636

Qy 83 GGGAGAGCGCACTGTCTCCGTGTGTAGCGCGCGCGAGCGGGCGCGAGCGGTGATCG 142
Db 637 GAGCGGGTGGCGCACTGTGTACAGCGCAGCGGGCGCGCAGAGAGAGAGCCCAAGTCT 696

Qy 143 GTCCCTTCGAACCTGGGAGGTCCAGTGGGTGCGTTAGGCCCAAGCCCCCAGCCCGGCT 202
Db 697 TCCAGGAGGGGCTCAGGGGGTCCCGAGGAGTCTCTCCCGGAGCAACACCCCTCTCCGGG 756

Qy 203 CCAAAAGCTCCAGGGCTCCCCAG 227
Db 757 CTTGATGTCGGCACCCCCCAGCCTG 781

RESULT 9
US-10-750-185-46989
; Sequence 46989, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46989
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Bovine
; ORGANISM: Bovine 19866880829104
US-10-750-185-46989

Query Match          3.1%; Score 39; DB 6; Length 1931;
Best Local Similarity 52.8%; Pred. No. 0.27;
Matches 84; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 54 CGAGTGAAGCTGGAGTTCCGGGGTGGCGGGAGGCGACTGTCCGTGGTCTGAGCGCC 113
Db 1745 CGAGAGGCGCTGGAGTCAACCACCTTCATGGGGGACAGCTGCCACCGCGCTCTGCAAG 1804

Qy 114 GCGAGAGCGGGCGCGAGCGGTGATCGGCTCCCTCGAACTGGGGAGGTCACATGGGGGT 173
Db 114 GCGAGAGCGGGCGCGAGCGGTGATCGGCTCCCTCGAACTGGGGAGGTCACATGGGGGT 173
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Db	1805	AAGAGGAACAGGCTCAGAGCTGGAGATGGGNTACACAGGCGCCTAGGTACAGTAGGCC	1864
Qy	174	CGCTTAGGGCCCCAAGGCCCCCACC	212
Db	1865	CTCTGAGACTGGAGAGCCCTCCCGGCTTCATACCCCC	1903

RESULT 10
US-10-507-928-9
; Sequence 9, Application US/10507928
; Publication No. US20050266024A1

```

; GENERAL INFORMATION:
; APPLICANT: POWDERMED LIMITED AND GLAXO GROUP LIMITED
;
; TITLE OF INVENTION: ADJUVANT
;
; FILE REFERENCE: N.88232B GCW
;
; CURRENT APPLICATION NUMBER: US/10/507,928
;
; CURRENT FILING DATE: 2004-09-17
;
; NUMBER OF SEQ ID NOS: 12
;
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 9
;
; LENGTH: 1689
;
; TYPE: DNA
;
; ORGANISM: Artificial sequence
;
; FEATURE:
;
; OTHER INFORMATION: nucleotide sequence of RT insert
US-10-507-928-9

```

	Query Match	3.0%;	Score 38;	DB 6;	Length 1689;
	Best Local Similarity	62.8%;	Pred. No. 0.49;		
	Matches 59;	Conservative 0;	Mismatches 35;	Indels 0;	Gaps 0;
Qy	623	AGTGGAGAGCCCCCTTTACAGGGGGCCCTGACAGTGGAAATGGCAGCAAGGACCTGCAGACG	682		
Db	278	AGCTGGGCATCCCCCATCCGCGCGCCCTGAGAAAGAGAGCGTGACCGTGTGGACG	337		
Qy	683	TGTCCATCACTGTGCTCAAGCTCACTCTGACGA	716		
Db	338	TGGCGCAGCGTTACTTCAGCGTCCCTTGGACGA	371		

```

RESULT 11
US-10-507-928-11
; Sequence 11, Application US/10507928
; Publication No. US20050266024A1
; GENERAL INFORMATION:
; APPLICANT: POWDERED LIMITED AND GLAXO GROUP LIMITED
; TITLE OF INVENTION: ADJUVANT
; FILE REFERENCE: N.88232B GCW
; CURRENT APPLICATION NUMBER: US/10/507,928
; CURRENT FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence of the coding insert in p73i-RT3
US-10-507-928-11

```

	Query Match	3.0%;	Score 38;	DB 6;	Length 1689;
	Best Local Similarity	62.8%;	Pred. No. 0.49;		
	Matches 59;	Conservative 0;	Mismatches 35;	Indels 0;	Gaps 0;
Qy	623	AGGTGGAGAGCCCCCTTTTCAGGGGGCCCTGCACTGGAATGGCAGCAAGGACCTGCAGGACG	682		
Db	278	AGCTGGGCATCCCCCATCCGCCCGCCCTGAAAGAGAAGAGCGTGACCGTGTGGACG	337		
Qy	683	TGTCATCACTGTGCTCAACGCTCACTCTTGAACGA	716		
Db	338	TGGCGCAGCGTTACTTTCAGCGTCCCTCTGGAACGA	371		

```

RESULT 12
US-11-029-465-9
; Sequence 9, Application US/11029465
; Publication No. US20050256070A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Ralph P.
; APPLICANT: Thomsen, Lindy
; APPLICANT: Van-Wely, Catherine
; APPLICANT: Ertl, Peter
; TITLE OF INVENTION: Adjuvant
; FILE REFERENCE: 033267-015
; CURRENT APPLICATION NUMBER: US/11/029,465
; CURRENT FILING DATE: 2005-01-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence
US-11-029-465-9

```

	Query Match	3.0%;	Score 38;	DB 7;	Length 1689;
	Best Local Similarity	62.8%;	Pred. No. 0.49;		
	Matches 59;	Conservative 0;	Mismatches 35;	Indels 0;	Gaps 0;
Qy .	623	AGGTGGAGAGCCCTTTTCAGGGGCGCTGCAGTGGAAATGCGACGAAGGACCTGCGAGACG	682		
Db	278	AGCTGGGCATCCCCCATCCGCGCGGCTGGAAGAAGAAGAGCGTGACCGTGTGGACG	337		
Qy	683	TGTCCTCATCTGTGCTCAAGCTCACTCTGAACGA	716		
Db	338	TGGCGCAGCGTTTACTTCAGCGTCCCTCTGACGA	371		

```

RESULT 13
; Sequence 11 Application US/11029465
; Publication No. US20050256070A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Ralph P.
; APPLICANT: Thomsen, Lindy
; APPLICANT: Van-Wely, Catherine
; APPLICANT: Ertl, Peter
; TITLE OF INVENTION: Adjuvant
; FILE REFERENCE: 033267-015
; CURRENT APPLICATION NUMBER: US/11/029,465
; CURRENT FILING DATE: 2005-01-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence o
; OTHER INFORMATION: p73i-RT3
US-11-029-465-11

```

	Query Match	3.0%	Score 38;	DB 7;	Length 1689;
	Best Local Similarity	62.8%	Pred. No. 0.49;		
	Matches 59;	Conservative	0;	Mismatches 35;	Indels 0;
					Gaps 0;
Qy	623	AGGTGAGAGCCCTTTTCAGGGCGCTGCAGTGGAAATGCGAGCAAGGACCTGCGAGACG	682		
Db	278	AGCTGGGCATCCCGCCATCCGGCGCGCTGAAGAAGAAGAGCGTGACCGTGTGACG	337		
Qy	683	TGTCCATCATGTGCTCAAGCTCACTCTGAACGA	716		
Db	338	TGGCGCAGCTTACTTCAGGCGTCCCTCTGACCA	371		

Job time : 345 secs

```
RESULT 14
US-11-121-086-29/c
; Sequence 29, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; PRIOR FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 160226
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-29

Query Match      3.0%; Score 37.8; DB 7; Length 160226;
Best Local Similarity 52.2%; Pred. No. 3.2;
Matches 84; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY      49 GGGCGCGAGTGGAGCTGGAGTTCGGGGTGGGGGGGAGGGGAGCTGTCCGTGGTCTGA 108
      |||||
Db      141257 GGCACAGCGGGGGGGGGGGGGGGGGGGAGGGGGGGGGGGGGGGGGGGGGGG 141198

QY      109 GCGCGCGGAGAGCGGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGT 168
      |||||
Db      141197 GGGAGCGGTGGAGGGGCTGGGGAGGAGGAAGGACGTACAGGGGAGGGGGGGCAGGG 141138

QY      169 GGGGTGCTTAGGGGCCAAAGCCCCCACCCTCCGCTCCAAAAG 209
      |||||
Db      141137 CGGGGCGCGGAGACCCCGCCCGCCCGCGCGCCCTTAAAG 141097

RESULT 15
US-11-121-086-62
; Sequence 62, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 200628
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-62

Query Match      3.0%; Score 37.8; DB 7; Length 200628;
Best Local Similarity 60.0%; Pred. No. 3.5;
Matches 63; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY      1128 CTTCCCTTCATGCATCCATTGTTGTTTCATTCATTCATCATCATCCACTGCCTCTG 1187
      |||||
Db      163254 CATCCATCCATCCATCCATCCATCTATCCATTCGTCATCCATCCATTCACCTACTATCC 163313

QY      1188 AGCTTTACCTCTGACTCCCTAACCTCCATCCAGACCTCTACGCACC 1232
      |||||
Db      163314 ATCCATCATCCATTCATTCACCCACCCATCACTCATTCATCCATC 163358
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Result No.	Score	Query Match	Length	DB	ID	Description	
C	1	44.8	11.9	11558	6	PTC-US93-06251-23	Sequence 23, Appl
	2	42	11.2	9822	3	US-09-949-016-15003	Sequence 15003, A
	3	41	10.9	1097	3	US-09-771-161A-58	Sequence 58, Appl
	4	41	10.9	3382	3	US-09-771-161A-59	Sequence 59, Appl
	5	40.4	10.8	6651	3	US-09-902-540-4944	Sequence 4944, Ap
	6	40.4	10.8	30780	3	US-09-902-540-1243	Sequence 1243, Ap
	7	40.2	10.7	2802	3	US-09-949-016-1335	Sequence 1335, Ap
	8	40.2	10.7	2806	3	US-09-688-188B-102	Sequence 102, App
	9	40.2	10.7	2806	3	US-09-291-417D-102	Sequence 102, App
	10	40.2	10.7	2838	3	US-09-949-016-794	Sequence 794, App
C	11	40.2	10.7	57559	3	US-09-949-016-13077	Sequence 13077, A
	12	40.2	10.7	57560	3	US-09-949-016-12536	Sequence 12536, A
	13	40	10.7	21295	3	US-09-902-540-1194	Sequence 1194, Ap
	14	39.2	10.5	6191	3	US-09-949-016-124631	Sequence 124631, A
	15	39.2	10.5	8374	3	US-09-949-016-15257	Sequence 15257, A
	16	39.2	10.5	45225	3	US-09-949-016-12428	Sequence 12428, A
	17	39.2	10.5	45226	3	US-09-949-016-13654	Sequence 13654, A
	18	39	10.4	30635	3	US-09-949-016-16501	Sequence 16501, A
	19	39	10.4	43414	3	US-09-949-016-12839	Sequence 12839, A
	20	39	10.4	43415	3	US-09-949-016-16491	Sequence 16491, A
C	21	38.8	10.3	1941	3	US-09-902-540-4762	Sequence 4762, Ap
	22	38.8	10.3	26492	3	US-09-902-540-1234	Sequence 1234, Ap
	23	38.6	10.3	1940	3	US-09-718-032-1	Sequence 1, Appl
	24	38.6	10.3	1941	3	US-09-082-737-1	Sequence 1, Appl

```
Db 428 GCGAGGGCGGGTAGGGACCTTTTCAGAGCCAGGAGGGCTTTTCGGGGCGGTGGGGCGCGC 487
Qy 134 GCCTGATCGGCTCCTCGAACTGGGGAGGTCCAGTGGGTGCG-CTTAGGGCCCAAGCCC 192
Db 488 TCGGAGCGAGCGCGGCTCGAGCGGGTGCCTGCGGGAGTGTATGACAGCGCGC 547
Qy 193 CCACCCGCTCCAAAAGTCCACAGGGCTCCCGAGGACCGGTGCTCGGCCCTTCCTTCG 252
Db 548 CCGGCCGAAACCCGAGCGCCGCGGGCTCCACCGCGGCTCCCGCCCTCCCGCG 607

RESULT 2
US-09-949-016-15003/c
; Sequence 15003, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15003
; LENGTH: 9622
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-15003

Query Match 11.2%; Score 42; DB 3; Length 9622;
Best Local Similarity 49.5%; Pred. No. 0.53;
Matches 108; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

Qy 38 GAGCGAGCAGGGCGCGAGTGAAGTGGAGTTCCGGGGTGGCGGGAGGCGACTGTC 97
Db 7138 GCGTGAGGCCCTGCTGGAAGGGTCTGCTGCGGTAGGGCTCTGTTCATGCCACGA 7079

Qy 98 CGTGTCTGAGCCCGCGAGCGGCGGAGCGGCTGATCGGCTCCCTCGAATGG 157
Db 7078 TCTGCTGTGTGGTGGGCCAGCGCGGTGTAGGAAGCCATCATGCCCTCCATCGGCTGG 7019

Qy 158 GGAGTCCAGTGGGTGCTTTAGGGCCCAAGCGCCCAAGCGGCTCCAAAAGCTCCCAAG 217
Db 7018 ACAGGACCTCTGGGGGACAGTAGCCCTTACCCCTGCTGTCCAGGCCCTCCACG 6959

Qy 218 GCCTCCCGAGCAGCGGTGCTCGGCCCTTCCTTCGGTC 255
Db 6958 TACACCCAGCAGCCTCCCTTCTGATCTCTCTTGGAC 6921

RESULT 3
US-09-771-161A-58
; Sequence 58, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
```

```
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 58
; LENGTH: 1097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-161A-58

Query Match 10.9%; Score 41; DB 3; Length 1097;
Best Local Similarity 52.0%; Pred. No. 0.75;
Matches 92; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 1 CCCTCCCTTCGAGCTGAGCTTACCTCTGGCGCAAAACAGCGAGGCGCGAGTGG 60
Db 23 CCCCCGCTCGGGCTGTGAGCGGCTCGGGGCGGGGGTGGCGCGGTGCGCGGCGG 82

Qy 61 AAGCTGAGTTCCGGGGTGGCGGGAGGAGGACTGTCCGTGGTGTCTAGCGCCGCGAGA 120
Db 83 CCGACGCTCCTCTTCGGCGCGCGCGCGGCGCATGCGTGGGGCGCGCGGTGGGGCG 142

Qy 121 GCGGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGTGCT 177
Db 143 GCGGGCGCGAGTTGCTTCCTCCGGGCGCGGCTGAGGGCCCCCGCGCGCGCGCT 199

RESULT 4
US-09-771-161A-59
; Sequence 59, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 59
; LENGTH: 3382
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: "
; LOCATION: (1)..(3382)
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'
US-09-771-161A-59

Query Match 10.9%; Score 41; DB 3; Length 3382;
Best Local Similarity 52.0%; Pred. No. 0.83;
Matches 92; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 1 CCCTCCCTTCGAGCTGAGCTTACCTCTGGCGCAAAACAGCGAGGCGCGAGTGG 60
Db 23 CCCCCGCTCGGGCTGTGAGCGGCTCGGGGCGGGGGTGGCGCGGTGCGCGGCGG 82

Qy 61 AAGCTGAGTTCCGGGGTGGCGGGAGGAGTGTCCGTGGTGTCTAGCGCCGCGAGA 120
Db 83 CCGACGCTCCTCTTCGGCGCGCGCGCGGCGCATGCGTGGGGCGCGCGGTGGGGCG 142

Qy 121 GCGGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGTGCT 177
Db 143 GCGGGCGCGAGTTGCTTCCTCCGGGCGCGGCTGAGGGCCCCCGCGCGCGCGCT 199

RESULT 5
US-09-902-540-4944
; Sequence 4944, Application US/09902540
```

Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 4944
LENGTH: 6651
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-4944

Query Match 10.8%; Score 40.4; DB 3; Length 6651;
Best Local Similarity 51.3%; Pred. No. 1.2;
Matches 120; Conservative 0; Mismatches 111; Indels 3; Gaps 1;

Qy 39 AGCGAGCGGGCGCGAGTGGAGCTGGAGTTCGGGGTGGGGGAGCGGAGCTGTC 98
Db 4498 ATCGAGCGAGGGCGCTCGAGCGCGGTGTCGCGACACGCGGATGAAGCACGGGGCC 4557

Qy 99 GTGTGCTGAGCGCGCGGAGAGCGGGCGCGGAGCGGTGATCGGCTCCCTCGAACTGGG 158
Db 4558 CTGAGCTG---CTCTTCCTGACCGCGCGGTGTCGCGGATGAGCGCCCTGTCGTGGCGAG 4614

Qy 159 GAGTCCAGTGGGTGCTTAGGGCCCAAGCCCGGCTCCAAAGCTCCCAAGG 218
Db 4615 GTGGAGCTGTGAGTCTGTGCTGCTGCGGCGCGGCGGTGCTGCTCAATG 4674

Qy 219 CTTCCCGAGCGGTGCTCGGCGCTTCTTCGCTGAGAAAGCTCCCAAGG 272
Db 4675 TCGGGAGCTGTTTCGCGGGGATGCTCAAGTCCATCGGGCGGGAAGTGCCTGCGCCG 4728

RESULT 6
US-09-902-540-1243
Sequence 1243, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1243
LENGTH: 30780
TYPE: DNA
ORGANISM: Myxococcus xanthus
FEATURE:
NAME/KEY: unsure
LOCATION: (1)...(30780)
OTHER INFORMATION: unsure at all n locations
US-09-902-540-1243

Query Match 10.8%; Score 40.4; DB 3; Length 30780;
Best Local Similarity 51.3%; Pred. No. 1.4;
Matches 120; Conservative 0; Mismatches 111; Indels 3; Gaps 1;

Qy 39 AGCGAGCGGGCGCGAGTGGAGTTCGGGGTGGGGGAGCGGAGCTGTC 98
Db 28499 ATCGAGCGAGGGCGCTCGAGCGCGGTGTCGCGGACACGCGGATGAAGCACGGGGCC 28558

Qy 99 GTGTGCTGAGCGCGCGGAGACGCGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGG 158
Db 28559 CTGAGCTG---CTCTTCCTGAGCGCGCGGTGTCGCGGATGAGCGCTGTCGTGGCGAG 28615

Qy 159 GAGTCCAGTGGGTGCTTAGGGCCCAAGCCCGGCTCCAAAGCTCCCAAGG 218
Db 28616 GTGGAGCTGGTGAATGTCGTCATTTGGCGTGTGGGCGGCGGCTGCTGCAATG 28675

Qy 219 CTTCCCGAGCGGTGCTCGGCGCTTCTTCGCTGAGAAAGCTCGGCGGCTGG 272
Db 28676 TCGGGAGCTGTTTCGCGGGGATGCTCAAGTCCATCGGGCGGGAAGTGCCTGCGCCG 28729

RESULT 7
US-09-949-016-1335
Sequence 1335, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1335
LENGTH: 2802
TYPE: DNA
ORGANISM: Human
US-09-949-016-1335

Query Match 10.7%; Score 40.2; DB 3; Length 2802;
Best Local Similarity 49.8%; Pred. No. 1.3;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Qy 23 ACCCTGGCGCAAAACGAGCGAGGCGGCGCGAGTGGAGTTCGCGGGTGGGC 82
Db 569 ACCACGCCACAGAGGGGGCGCCAGGAGGAGGAGGCGCGGTTCCGCGGTACAGC 628

Qy 83 GGGAGCGGAGTCTGCTGCTGCTGAGCGCGCGGAGAGCGGCGGAGGCGGCTGATCG 142
Db 629 GAGGCGGGTGGCGGCGAGTGTGTGACGCGGCGGCGGCGGAGAGAGGCGGCTCT 688

Qy 143 GCTCCCTCGAACTGGGAGGTCCAGTGGGGTTCCTTAGGGCCCAAGCGCCCGGCT 202
Db 689 TCAGGAGGGGCTCAGGGGTCCCGAGGAGTCTCCCGGAGCAACACGCCCCCTCTCGGG 748

Qy 203 CCAAAAGCTCCCGAGGCGCTCCCGAG 227
Db 749 CCTGATGTCGGCACCCCGGAGCCTG 773

RESULT 8
US-09-688-188B-102
Sequence 102, Application US/09688188B
Patent No. 6656716
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0328
CURRENT APPLICATION NUMBER: US/09/688,188B
CURRENT FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 09/291,417

; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 2806
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-688-188B-102

Query Match 10.7%; Score 40.2; DB 3; Length 2806;
Best Local Similarity 49.8%; Pred. No. 1.3;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 23 ACCCTGGCGCAACGACGAGGAGGCGGCGCGAGTGGAGCTGGAGTTCGGGGTGGGC 82
DB 567 ACCACGGCCAGAGGGGGCCAGGGAAGCAGCAGCGAGGCGGTTTCGCGGTTCACAGC 626

QY 83 GGGGAGGCGACTGTCCGTGTGCTGAGCGCGCGGAGAGCGGCGCGAGCGGCTGATCG 142
DB 627 GAGCGGGTGGCGAGTGTGTACAGGCGACGGCGGGGCCAGAGAGAGGCCCAAGTCT 686

QY 143 GCTCCCTCGAACTGGGGAGGTCCAGTGGGTGCTTAGGGCCCAAAGCCCCACCCGGCT 202
DB 687 TCCAGGAGGGCTCAGGGGGTCCCGAGGAGTCTCTCCGGGACAAAGCCCCCTCTCCGGG 746

QY 203 CCAAAAGCTCCAGGGCTCCCGCAG 227
DB 747 CTGATGTGCGCACCCCCCAGCCTG 771

RESULT 9

US-09-291-417D-102
; Sequence 102, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 2806
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-291-417D-102

Query Match 10.7%; Score 40.2; DB 3; Length 2806;
Best Local Similarity 49.8%; Pred. No. 1.3;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 23 ACCCTGGCGCAACGACGAGGAGGCGGCGCGAGTGGAGTTCGGGGTGGGC 82
DB 567 ACCACGGCCAGAGGGGGCCAGGGAAGCAGCAGCGAGGCGGTTTCGCGGTTCACAGC 626

QY 83 GGGGAGGCGACTGTCCGTGTGCTGAGCGCGCGGAGAGCGGCGCGAGCGGCTGATCG 142
DB 627 GAGCGGGTGGCGAGTGTGTACAGGCGACGGCGGGGCCAGAGAGAGGCCCAAGTCT 686

QY 143 GCTCCCTCGAACTGGGGAGGTCCAGTGGGTGCTTAGGGCCCAAAGCCCCACCCGGCT 202
DB 687 TCCAGGAGGGCTCAGGGGGTCCCGAGGAGTCTCTCCGGGACAAAGCCCCCTCTCCGGG 746

QY 203 CCAAAAGCTCCAGGGCTCCCGCAG 227
DB 747 CTGATGTGCGCACCCCCCAGCCTG 771

RESULT 10

US-09-949-016-794
; Sequence 794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 794
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-794

Query Match 10.7%; Score 40.2; DB 3; Length 2838;
Best Local Similarity 49.8%; Pred. No. 1.3;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 23 ACCTGGGCGCAACGACGAGGAGGCGGCGCGAGTGGAGTTCGGGGTGGGC 82
DB 577 ACCACGGCCAGAGGGGGCCAGGGAAGCAGCAGCGAGCGGTTTCGCGGTTCACAGC 636

QY 83 GGGGAGGCGACTGTCCGTGTGCTGAGCGCGCGGAGAGCGGCGCGAGCGGCTGATCG 142
DB 637 GAGCGGGTGGCGAGTGTGTACAGGCGACGGCGGCGGCGCAGAGAGAGGCCCAAGTCT 696

QY 143 GCTCCCTCGAACTGGGGAGGTCCAGTGGGTGCTTAGGGCCCAAAGCCCCACCCGGCT 202
DB 697 TCCAGGAGGGCTCAGGGGGTCCCGAGGAGTCTCTCCGGGACAAAGCCCCCTCTCCGGG 756

QY 203 CCAAAAGCTCCAGGGCTCCCGCAG 227
DB 757 CTGATGTGCGCACCCCCCAGCCTG 781

RESULT 11

US-09-949-016-13077
; Sequence 13077, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13077
; LENGTH: 57559
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13077

Query Match 10.7%; Score 40.2; DB 3; Length 57559;
Best Local Similarity 49.8%; Pred. No. 1.7;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 23 ACCCTGGCGCCAAACGAGCGAGCGGCGCGAGTGGAGCTGCCGGGTGGGC 82
DB ACCAGGCCAGAGGGGCCCAAGGAGCGAGCGCGGCTTCGGCGGTACAGC 49295

QY 83 GGGAGGCGCACTGTCCTGTGTCTGAGCGCGCGGAGAGCGGCGCGGCTGATCG 142
DB GAGCGGGTGGCGCACTGTCAGCAGCGAGCGGCGGCGGCGAGAGAGCCCAAGTCT 49355

QY 143 GCTCCCTCGAACTCGGAGGTCCAGTGGGTGCTTAGGGCCCAAGCCCCCAGCGGCT 202
DB TCAGGGAGGGCTCAGGGGGTCCCGAGGAGTCTCCCGGGAGCAACGCCCTCTCCGGG 49415

QY 203 CCAAAAGCTCCAGGGGCTCCCCAG 227
DB CCTGATGTCGCACACCCCGGAGCTG 49440

RESULT 12
US-09-949-016-12536
; Sequence 12536, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12536
; LENGTH: 57560
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12536

Query Match 10.7%; Score 40.2; DB 3; Length 57560;
Best Local Similarity 49.8%; Pred. No. 1.7;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 23 ACCCTGGCGCCAAACGAGCGAGCGGCGCGAGTGGAGCTGCCGGGTGGGC 82
DB ACCAGGCCAGAGGGGCCCAAGGAGCGAGCGCGGCTTCGGCGGTACAGC 49295

QY 83 GGGAGGCGCACTGTCCTGTGTCTGAGCGCGCGGAGAGCGGCGCGGCTGATCG 142
DB GAGCGGGTGGCGCACTGTCAGCAGCGAGCGGCGGCGGCGAGAGAGCCCAAGTCT 49355

QY 143 GCTCCCTCGAACTCGGAGGTCCAGTGGGTGCTTAGGGCCCAAGCCCCCAGCGGCT 202
DB TCAGGGAGGGCTCAGGGGGTCCCGAGGAGTCTCCCGGGAGCAACGCCCTCTCCGGG 49415

QY 203 CCAAAAGCTCCAGGGGCTCCCCAG 227
DB CCTGATGTCGCACACCCCGGAGCTG 49440

RESULT 13
US-09-902-540-1194
; Sequence 1194, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1194
; LENGTH: 21295
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1194

Query Match 10.7%; Score 40; DB 3; Length 21295;
Best Local Similarity 47.9%; Pred. No. 1.7;
Matches 115; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 45 GCAGGGCGCGAGTGGAAAGCTGGAGTTCCGGGGTGGGCGGGAGGCGACTGTCCGTGGTG 104
DB GGAGGAGAGGCGCGCTGGCAGCGCATCCAGGAGCTGCTCGGAGGGCGGGGGCGCGG 16314

QY 105 CTGAGCGCGCGAGAGCGGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTC 164
DB CGCAGCGCGCGCCACCGCGCGCGGGAAGCGCCCGGAGGCAACCGCGCTGGCGCGGG 16374

QY 165 CAGTGGGTGCTTAGGGCCCAAGCCCGCCCGCTCCAAAGCTCCAGGGCCTCCC 224
DB CTGGCGGAGAGCTGACGAAAGCGGCCCTTTGCGCACGGGCTCACGGTGGGAGCCT 16434

QY 225 CAGGCACCGGTGCTCGGCGCTTCTTTCGGTTCAGAAAGTCCGCCCTGGGGGCGATTGTC 284
DB CAGGGCGAGCGCTGAGTCCAAAGCGTGCAGAGTGGCGGCTTGTAGGCTCCGAC 16494

RESULT 14
US-09-949-016-124631
; Sequence 124631, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124631
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-124631

Query Match 10.5%; Score 39.2; DB 3; Length 601;
Best Local Similarity 48.2%; Pred. No. 1.9;
Matches 110; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 49 GGGCGGAGTGGAAAGCTGGAGTTCCGGGGTGGGCGGGAGGCGACTGTCTCGTGGTGTGA 108
DB GGGAGTGGGTGCCCAAGGGGGTCTGGCGGGTTCGAGAAGCGTCTGCTCCCTCGGACTCG 143

QY 109 GCGCCCGGAGAGCGGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCAGT 168
DB GCGCCCCCAGCCCTGGCGGGTCCCGCTGAGCGGCTGCCCCCTGCCCGGACACTGCT 203

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Qy 169 GGGGTGCTTAGGGCCCAAGCCCCACCGGCTCCAAAAGTCCACAGGCTCCCCCAGG 228
Db 204 CACCTCCCGGGGCGCTCGCCAGGCGGCCCTGCGTCCCGGGTCCCCCGGCTGCCCAGG 263
Qy 229 CACCGGTGCTCGGCCCTTCTTCCTCGGTGAGAAAGTCGCCCTCGGGGC 276
Db 264 GAGCGGAGTGGGTTCACAGCGGCCCGTGGCGCACKCCGGCTGGGC 311

RESULT 15
US-09-949-016-15257
; Sequence 15257, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15257
; LENGTH: 8374
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15257

Query Match 10.5%; Score 39.2; DB 3; Length 8374;
Best Local Similarity 48.2%; Pred. No. 2.5;
Matches 110; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

Qy 49 GGGCGCAGTGGAGCTGGAGTTCGGGGTGGCGGGAGGCGACTGTCCGTGTGCTGA 108
Db 5933 GGGAGTGGGTCCCCAAGGGGGTCTGTGGCGGTGCGAAGCGTCTCCCCCTCGGACTCG 5992
Qy 109 GCGCGCGCAGAGCGGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGT 168
Db 5993 GCGCCCCCAGCCCTGGCGGGTCCCGCTGAGCGGCTGCCCGTCCCGCGGCTGCCCAGG 6052
Qy 169 GGGGTGCTTAGGGCCCAAGCCCCACCGGCTCCAAAAGTCCACAGGCTCCCCCAGG 228
Db 6053 CACCTCCCGGGGCGCTCGCCAGGCGGCCCTGCGTCCCGGGTCCCCCGGCTGCCCAGG 6112
Qy 229 CACCGGTGCTCGGCCCTTCTTCCTCGGTGAGAAAGTCGCCCTCGGGGC 276
Db 6113 GAGCGGAGTGGGTTCACAGCGGCCCGTGGCGCACTCCGGCTGGGC 6160
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Search completed: December 13, 2005, 07:35:11
Job time : 88.9845 secs

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 07:13:57 ; Search time 428.232 Seconds
(without alignments)
7241.448 Million cell updates/sec

Title: US-09-977-579A-4_COPY_1_375
Perfect score: 375
Sequence: 1 cctcccttcgagctgagc.....gaagcgccagccccagaag 375

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	375	100.0	1261	3	US-09-977-579-4
2	375	100.0	1261	9	US-10-482-834A-22
3	361	96.3	651	4	US-09-925-065A-513769
4	360.6	96.2	651	4	US-09-925-065A-513767
5	360.6	96.2	651	4	US-09-925-065A-513768
6	45.2	12.1	497	7	US-10-424-599-133788
7	44.8	11.9	29340	7	US-10-322-281-642
8	43	11.5	396	7	US-10-437-963-98256
9	43	11.5	1021	7	US-10-767-701-11876
10	42.6	11.4	419	8	US-10-425-115-24179
11	42.2	11.3	1211	7	US-10-437-963-27585
12	41.4	11.0	696	7	US-10-437-963-90177
13	41.4	11.0	58038	8	US-10-741-600-17942
14	41.4	11.0	333811	8	US-10-741-600-17681
15	41.2	11.0	922	6	US-10-017-161-1435
16	41.2	11.0	922	6	US-10-292-798-1161
17	41	10.9	1097	3	US-09-771-161A-58
18	41	10.9	3382	3	US-09-771-161A-59
19	40.2	10.7	766	7	US-10-260-238-52
20	40.2	10.7	791	7	US-10-437-963-84059
21	40.2	10.7	1071	7	US-10-437-963-84064
22	40.2	10.7	2739	9	US-10-956-157-4971
23	40.2	10.7	2806	3	US-09-291-417-102

24	40.2	10.7	2806	8	US-10-725-329-102	Sequence 102, App
25	40.2	10.7	2806	9	US-10-725-121-102	Sequence 102, App
26	40.2	10.7	2811	9	US-10-450-763-19239	Sequence 19299, A
27	40.2	10.7	2838	6	US-10-134-102-3	Sequence 3, Appli
28	40.2	10.7	2838	9	US-10-956-157-1497	Sequence 1497, Ap
29	40.2	10.7	2838	10	US-11-045-182-1	Sequence 1, Appli
C 30	40.2	10.7	20000	6	US-10-188-777-11	Sequence 11, Appl
C 31	40	10.7	645	7	US-10-767-701-25929	Sequence 25929, A
C 32	40	10.7	940	7	US-10-437-963-40850	Sequence 40850, A
C 33	39.8	10.6	392	3	US-09-960-352-2238	Sequence 2238, Ap
C 34	39.8	10.6	863	7	US-10-437-963-71791	Sequence 71791, A
C 35	39.6	10.6	712	8	US-10-425-115-118813	Sequence 118813, A
C 36	39.6	10.6	1092	7	US-10-437-963-84061	Sequence 84061, A
C 37	39.6	10.6	1092	7	US-10-767-701-9739	Sequence 9739, Ap
C 38	39.6	10.6	4233	8	US-10-723-860-4143	Sequence 4143, Ap
C 39	39.6	10.6	4233	9	US-10-756-149-4115	Sequence 4115, Ap
C 40	39.5	10.6	4244	8	US-10-723-860-8016	Sequence 8016, Ap
41	39.2	10.5	600	9	US-10-972-079-6799	Sequence 6799, Ap
42	39.2	10.5	759	7	US-10-260-238-230	Sequence 230, App
43	39.2	10.5	972	8	US-10-425-115-17653	Sequence 17653, A
C 44	39.2	10.5	1294	7	US-10-437-963-73166	Sequence 73166, A
C 45	39.2	10.5	6888	8	US-10-602-494-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-09-977-579-4
; Sequence 4, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
; TITLE OF INVENTION: channel
; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977,579
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-977-579-4

Query Match	100.0%;	Score 375;	DB 3;	Length 1261;
Best Local Similarity	100.0%;	Pred. No. 9.5e-98;		
Matches 375;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CCCTCCCTTCGAGCTGAGCTTACCTCGGCGGAAACGAGCGAGGCGGCGGAGTGG	60	
Db	1	CCCTCCCTTCGAGCTGAGCTTACCTCGGCGGAAACGAGCGAGGCGGCGGAGTGG	60	
Qy	61	AAGCTGGAGTTCGCGGGTGGCGGGAGGCGAGTGTCCGTGGTGTCTGAGCGCCGCGAGA	120	
Db	61	AAGCTGGAGTTCGCGGGTGGCGGGAGGCGAGTGTCCGTGGTGTCTGAGCGCCGCGAGA	120	
Qy	121	CGCGGCGGAGCGGCTGATCGGCTCCCTGAACTGGGAGGTCCTAGTGGGTGCTTAG	180	
Db	121	CGCGGCGGAGCGGCTGATCGGCTCCCTGAACTGGGAGGTCCTAGTGGGTGCTTAG	180	
Qy	181	GGCCCAAGCCCCCACCCTCCAAAGTCCCAAGGCTCCAGGCGCTCCCGAGGTCGCTCG	240	
Db	181	GGCCCAAGCCCCCACCCTCCAAAGTCCCAAGGCTCCAGGCGCTCCCGAGGTCGCTCG	240	
Qy	241	GCCTTCCTTCGCTCAGAAAGTCCGCCCTCGGGGCGAGTTCGTCCCAAGGGTTTCCTCG	300	
Db	241	GCCTTCCTTCGCTCAGAAAGTCCGCCCTCGGGGCGAGTTCGTCCCAAGGGTTTCCTCG	300	

Db 241 GCCCTTCCTCGGTGAGAAAGTCGCCCTCGGGGCGAGTTCTGTCCTCCAAAGGGTTTCCTCG 300
Qy 301 AAAGAATCTGAGAGGGCGCAGTCTCTTGACCGAGGAATCTCTGTGTAGCCTTTGGGAAGC 360
Db 301 AAAGAATCTGAGAGGGCGCAGTCTCTTGACCGAGGAATCTCTGTGTAGCCTTTGGGAAGC 360
Qy 361 CGCCAGCCCCAGAAG 375
Db 361 CGCCAGCCCCAGAAG 375

RESULT 2
US-10-482-834A-22
; Sequence 22, Application US/10482834A
; Publication No. US20050074764A1
; GENERAL INFORMATION:
; APPLICANT: Mulley, John Charles
; APPLICANT: Harkin, Louise Anne
; APPLICANT: Dibbens, Michelle
; APPLICANT: Wallace, Robyn
; APPLICANT: Phillips, Hillary Anny
; APPLICANT: Heron, Sara Elizabeth
; APPLICANT: Berkovic, Samuel Frank
; APPLICANT: Scheffer, Ingrid Eileen
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
; FILE REFERENCE: 1386/17
; CURRENT APPLICATION NUMBER: US/10/482,834A
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-834A-22

Query Match 100.0%; Score 375; DB 9; Length 1261;
Best Local Similarity 100.0%; Pred. No. 9.5e-98;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTCCCTTCGAGCTGAGCTTACCCCTGGGGCGCAACAGCGAGCGAGGGCGCGAGTGG 60
Db 1 CCCTCCCTTCGAGCTGAGCTTACCCCTGGGGCGCAACAGCGAGCGAGGGCGCGAGTGG 60

Qy 61 AAGCTGAGATTCCGGGGTGGGGGAGGCGACTGTCCTGCTGAGTGTGAGCCCGCGGAGA 120
Db 61 AAGCTGAGATTCCGGGGTGGGGGAGGCGACTGTCCTGCTGAGTGTGAGCCCGCGGAGA 120

Qy 121 GCGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTGCCTTAG 180
Db 121 GCGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTGCCTTAG 180

Qy 181 GGCCCAAGAGCCCCACCCGGGTCCTCCAAAGCTCCCAAGGGCCTCCCGAGGCACCGGTGCTCG 240
Db 181 GGCCCAAGAGCCCCACCCGGGTCCTCCAAAGCTCCCAAGGGCCTCCCGAGGCACCGGTGCTCG 240

Qy 241 GCCCTTCCTTCGGTTCAGAAAGTGCCTCCCTGGGGGCGAGTTCGTCCCAAGGGTTTCCTCG 300
Db 241 GCCCTTCCTTCGGTTCAGAAAGTGCCTCCCTGGGGGCGAGTTCGTCCCAAGGGTTTCCTCG 300

Qy 301 AAAGAATCTGAGAGGGCGCAGTCTTGACCGAGGAATCTCTGTGTAGCCTTTGGGAAGC 360
Db 301 AAAGAATCTGAGAGGGCGCAGTCTTGACCGAGGAATCTCTGTGTAGCCTTTGGGAAGC 360

Qy 361 CGCCAGCCCCAGAAG 375
Db 361 CGCCAGCCCCAGAAG 375

RESULT 3
US-09-925-065A-513769
; Sequence 513769, Application US/09925065A

; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 513769
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-513769

Query Match 96.3%; Score 361; DB 4; Length 651;
Best Local Similarity 99.7%; Pred. No. 1e-93;
Matches 372; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 3 CTCCTTCGAGCTGAGCTTACCCCTGGGGCGCAACAGCGAGCGAGGGCGCGAGTGGAA 62
Db 131 CTCCTTCGAGCTGAGCTTACCCCTGGGGCGCAACAGCGAGCGAGGGCGCGAGTGGAA 189

Qy 63 GCTGAGTTCCGGGTGGGGGAGGCGACTGTCCTGCTGAGTGTGAGCGCGCGGAGAGC 122
Db 190 GCTGAGTTCCGGGTGGGGGAGGCGACTGTCCTGCTGAGTGTGAGCGCGCGGAGAGC 249

Qy 123 GGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTTCGTTAGGG 182
Db 250 GGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTTCGTTAGGG 309

Qy 183 CCCTCCCTTCGAGCTGAGCTTACCCCTGGGGCGCAACAGCTCCCGAGGGCTCCCGAGGCACCGGTGCTCGGC 242
Db 310 CCCTCCCTTCGAGCTGAGCTTACCCCTGGGGCGCAACAGCTCCCGAGGGCTCCCGAGGCACCGGTGCTCGGC 369

Qy 243 CTTTCCTTCGGTTCAGAAAGTGCCTCCCTGGGGGAGTTCGTCCCAAGGGTTTCCTCGAA 302
Db 370 CTTTCCTTCGGTTCAGAAAGTGCCTCCCTGGGGGAGTTCGTCCCAAGGGTTTCCTCGAA 429

Qy 303 AGAATCTGAGAGGGCGCAGTCTTGACCGAGGGAATCTCTGTGTAGCCTTTGGAAGCG 362
Db 430 AGAATCTGAGAGGGCGCAGTCTTGACCGAGGGAATCTCTGTGTAGCCTTTGGAAGCG 489

Qy 363 CCAGCCCCAGAAG 375
Db 490 CCAGCCCCAGAAG 502

RESULT 4
US-09-925-065A-513767
; Sequence 513767, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147

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; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513767
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-513767

Query Match          96.2%; Score 360.6; DB 4; Length 651;
Best Local Similarity 99.5%; Pred. No. 1.3e-93;
Matches 371; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 3 CTCCTTCCGAGCTGAGCTTACCTCGGCGCAAAACGAGCGAGCGGGCGCGAGTGGAA 62
DB 131 CTCCTTCCGAGCTGAGCTTACCTCGGCGCAAAACGAGCGA-GCAGGGGCGCGAGTGGAA 189

QY 63 GCTGGAGTTCCGGGTCGGGAGGCGACTGTCCTGCTGCTGAGCGCGCGGAGAGC 122
DB 190 GCTGGAGTTCCGGGTCGGGAGGCGACTGTCCTGCTGCTGAGCGCGCGGAGAGC 249

QY 123 GGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGTCGCTTAGGG 182
DB 250 GGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGTCGCTTAGGG 309

QY 183 CCCAAAGCCCCACCCGGCTCCAAAGCTCCAGGGGCTCCCAAGGACACCGGTCTCGGC 242
DB 310 CCCAAAGCCCCACCCGGCTCCAAAGCTCCAGGGGCTCCCAAGGACACCGGTCTCGGC 369

QY 243 CCTTCTTCGGTCAGAAAGTCGCCCCCTGGGGGAGTTCGTCCTCGAA 302
DB 370 CCTTCTTCGGTCAGAAAGTCGCCCCCTGGGGGAGTTCGTCCTCGAA 429

QY 303 AGAATCTGAGAGGCGCAGTCCCTTGACCGAGGAATCTCTGTGTAGCTTGGAGCCG 362
DB 430 AGAATCTGAGAGGCGCAGTCCCTTGACCGAGGAATCTCTGTGTAGCTTGGAGCCG 489

QY 363 CCAGCCCCAGAAG 375
DB 490 CCAGCCCCAGAAG 502
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RESULT 5
US-09-925-065A-513768
; Sequence 513768, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513768
; LENGTH: 651
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-513768

Query Match          96.2%; Score 360.6; DB 4; Length 651;
Best Local Similarity 99.5%; Pred. No. 1.3e-93;
Matches 371; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 3 CTCCTTCCGAGCTGAGCTTACCTCGGCGCAAAACGAGCGAGCGGGCGCGAGTGGAA 62
DB 131 CTCCTTCCGAGCTGAGCTTACCTCGGCGCAAAACGAGCGA-GCAGGGGCGCGAGTGGAA 189

QY 63 GCTGGAGTTCCGGGTCGGGAGGCGACTGTCCTGCTGCTGAGCGCGCGGAGAGC 122
DB 190 GCTGGAGTTCCGGGTCGGGAGGCGACTGTCCTGCTGCTGAGCGCGCGGAGAGC 249

QY 123 GGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGTCGCTTAGGG 182
DB 250 GGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGTCGCTTAGGG 309

QY 183 CCCAAAGCCCCACCCGGCTCCAAAGCTCCAGGGGCTCCCAAGGACACCGGTCTCGGC 242
DB 310 CCCAAAGCCCCACCCGGCTCCAAAGCTCCAGGGGCTCCCAAGGACACCGGTCTCGGC 369

QY 243 CCTTCTTCGGTCAGAAAGTCGCCCCCTGGGGGAGTTCGTCCTCGAA 302
DB 370 CCTTCTTCGGTCAGAAAGTCGCCCCCTGGGGGAGTTCGTCCTCGAA 429

QY 303 AGAATCTGAGAGGCGCAGTCCCTTGACCGAGGAATCTCTGTGTAGCTTGGAGCCG 362
DB 430 AGAATCTGAGAGGCGCAGTCCCTTGACCGAGGAATCTCTGTGTAGCTTGGAGCCG 489

QY 363 CCAGCCCCAGAAG 375
DB 490 CCAGCCCCAGAAG 502
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RESULT 6
US-10-424-599-133788/c
; Sequence 133788, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 133788
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(497)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_91816C.1
US-10-424-599-133788

Query Match          12.1%; Score 45.2; DB 7; Length 497;
Best Local Similarity 54.6%; Pred. No. 0.0033;
Matches 89; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 38 GAGCGAGCGAGCGCGCGAGTGGAAAGTGGAGTTCGGGGTGGCGGGGAGGCGACTGTC 97
DB 301 GGGGGGGAGGGGGGGGGGGGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 242

QY 98 CGTGGTGTGAGCGCGCGGCGAGAGCGGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGG 157
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; SEQ ID NO 24179
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(419)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_122057C.1
US-10-425-115-24179

Query Match 11.4%; Score 42.6; DB 8; Length 419;
Best Local Similarity 51.7%; Pred. No. 0.019;
Matches 119; Conservative 0; Mismatches 110; Indels 1; Gaps 1;
QY 56 AGTGAAGCTTGAGTTCCGGGTGGCGGGAGCGGAGCTGTCCGTGTGCTGAGCGCGG 115
DB 371 AGTCTAGCGCGGAGAGTGGGTGCTGCTTCCGACGGGGGGGGGG 312
QY 116 CGAGAGCGGGCGGAGCGGTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTCG 175
DB 311 GGAGACCGAGCGGAAGCGGGCGGCGAGCACCACTGTCTGGGCGAGGCCAGCCCGCG 252
QY 176 CTTAGGCGCCAAAGCCCGCCACCGGCTCCAAAAGCTCCGAGGGCTCCCGAGCACCGGT 235
DB 251 TGGAGGCCCGCCAGCGGAGCGGAGAGCACCGGAGCGGCCCGCGGAGGGGCGAGGA 192
QY 236 GCTCGGCGCT-TCCCTTCGGTCAGAAAGTCGCCCGCTCGGGGCGAGTTCGTC 284
DB 191 GCTTAGCGANGTCCGCCGCCAGTAGGACTCGGCCCTTGAGGTTGGCCGCC 142

RESULT 11

US-10-437-963-27585/c
; Sequence 27585, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 27585
; LENGTH: 1211
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_32265C.1
US-10-437-963-27585

Query Match 11.3%; Score 42.2; DB 7; Length 1211;
Best Local Similarity 55.9%; Pred. No. 0.023;
Matches 80; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 40 GCGAGGCGAGGGGCGGAGTGAAGCTCGAGTTCGGGGGTGGCGGGGAGCGAGCTGTCCG 99
DB 204 GCGCGGGGGGGGGGGGGGGGGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 145
QY 100 TGGTGTGAGCGCGCGGCGAGAGCGGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGG 159
DB 144 GGGGCGGGCGCCCGGG 85
QY 160 AGGTCCAGTGGGTTCGCTTAGG 182

DB 84 GGGCGCGCGGGGGCGCGGGGG 62

RESULT 12

US-10-437-963-90177/c
; Sequence 90177, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 90177
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_88871C.1
US-10-437-963-90177

Query Match 11.0%; Score 41.4; DB 7; Length 696;
Best Local Similarity 48.5%; Pred. No. 0.04;
Matches 114; Conservative 0; Mismatches 121; Indels 0; Gaps 0;
QY 10 CCGAGCTGAGCTTACCTCTGGGCGCAACGAGCGAGGCGGGGCGCGAGTGAAGCTGGAG 69
DB 594 CGGCGGGCGCGACCGAGCGCGGGATGCGAGCGCGGAGCGCGGAGGTTGGCCCGTGC 535
QY 70 TTCGGGGTGGCGGGAGCGGACTGTCTCGTGTGTCTGAGCGCGCGGAGAGCGGGCGCG 129
DB 534 GGTGAGCGCCAGCGCGGGCGCGCGCGGCGGCGGAGGCGCGGCGGCGGAGGCCCGTC 475
QY 130 GAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTTCGTTAGGGCCCCAAG 189
DB 474 GAGCGCAACAGCGCGCGCGGGGATGCGTGTGGGGCCCACTGTCTGGGGCCG 415
QY 190 CCCCCACCGGCTCCAAAAGCTCCAGGGGCTCCCGAGGACCGGTCGTCGGGCC 244
DB 414 TCCCTTCTCTCCAGCGGAGCGCGCGCGCTCAACCGCGCGCGCGCGCGCTCC 360

RESULT 13

US-10-741-600-17942
; Sequence 17942, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17942
; LENGTH: 58038
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-17942
Query Match 11.0%; Score 41.4; DB 8; Length 58038;
Best Local Similarity 49.8%; Pred. No. 0.032;

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Matches 132; Conservative 1; Mismatches 127; Indels 5; Gaps 1;
Qy 28 GGGCGCAACAGCAGCAGCGCGCGCGAGCTGGAGTTCGGGGTGGCGGGGA 87
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6432 GGACRCACGGGGCTTGGCGACGGCGGCGAGTGCCCGAGGAGCGCGCTTCGGGGCGGGG 6491
Qy 88 GGCGACTGTCGCTGGTGTCTAGCGCCGCGAGCGCGCGGCGAGCGCTGATCGGCTCC 147
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6492 GCCGGGTGTCCTTCCGCGGGCTCAGGGTGGAGCGGTGCACGGCTGTTTCGC- 6550
Qy 148 CTCGAACCTGGGAGGTCCAGTGGGGTGCCTTAGGGCCCAAGCCCAACCGGCTCCAAA 207
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6551 ----ACCCCTCGCGCCCTCTGGCCCGCGCGGGGCCCTTTACGGGACCTCCCCACA 6606
Qy 208 AGCTCCAGGCGCTCCCGACGCGGTGCTCGGCCCTCTCTCGGTGAGAAAGTCGCC 267
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6607 AGACTCAAGGCTCGCGGGGCACTCGCTCTCCGCCCTTCCCGGAATCCAAACTTCCCTC 6666
Qy 268 CTGGGGGCGAGTTCGTCCCAAGGG 292
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6667 TGCAGCGCGCGCTTTCACGGAGGG 6691

RESULT 14
US-10-741-600-17681
; Sequence 17681, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17681
; LENGTH: 333811
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)..(333811)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17681

Query Match 11.0%; Score 41.4; DB 8; Length 333811;
Best Local Similarity 49.8%; Pred. No. 0.029;
Matches 132; Conservative 1; Mismatches 127; Indels 5; Gaps 1;
Qy 28 GGGCGCAACAGCAGCAGCGCGCGCGAGTGGAGTTCGGGGTGGCGGGGA 87
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
191325 GGACRCACGGGGCTTGGCGACGGCGGCGAGTGCCCGAGGAGCGCGGTTCGGGGCGGGG 191384
Qy 88 GGCGACTGTCGCTGGTGTCTAGCGCCGCGAGCGCGGCGGCGAGCGCTGATCGGCTCC 147
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
191385 GCCGGGTGTCCTTCCGCGGGCTCAGGGTGGAGGGCGGTGCAGCGGTCTGTTTCGC- 191443
Qy 148 CTCGAACCTGGGAGGTCCAGTGGGGTGCCTTAGGGCCCAAGCCCAACCGGCTCCAAA 207
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
191444 ----ACCCCTCGCGCCCTCTGGCCCGCGGGGCCCTTTACGGGACCTCCCCACA 191499
Qy 208 AGCTCCAGGCGCTCCCGACGCGGTGCTCGGCCCTCTCTCGGTGAGAAAGTCGCC 267
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
191500 AGACTCAAGGCTCGCGGGGCACTCGCTCTCCGCCCTTCCCGGAATCCAAACTTCCCTC 191559
Qy 268 CTGGGGGCGAGTTCGTCCCAAGGG 292
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
191560 TGCAGCGCGCGCTTTCACGGAGGG 191584

RESULT 15
US-10-017-161-1435
; Sequence 1435, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABEURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1435
; LENGTH: 922
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: source
; LOCATION: (1)..(922)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(722)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(26)
; OTHER INFORMATION: a, t, c, g, unknown or other
; NAME/KEY: modified_base
; LOCATION: (62)
; OTHER INFORMATION: a, t, c, g, unknown or other
; NAME/KEY: modified_base
; LOCATION: (124)..(125)
; OTHER INFORMATION: a, t, c, g, unknown or other
; NAME/KEY: modified_base
; LOCATION: (127)..(128)
; OTHER INFORMATION: a, t, c, g, unknown or other
; NAME/KEY: modified_base
; LOCATION: (131)
; OTHER INFORMATION: a, t, c, g, unknown or other
; NAME/KEY: modified_base
; LOCATION: (133)..(134)
; OTHER INFORMATION: a, t, c, g, unknown or other
; NAME/KEY: modified_base
; LOCATION: (138)
; OTHER INFORMATION: a, t, c, g, unknown or other
; NAME/KEY: modified_base
; LOCATION: (142)..(145)
; OTHER INFORMATION: a, t, c, g, unknown or other
; NAME/KEY: modified_base
; LOCATION: (147)
; OTHER INFORMATION: a, t, c, g, unknown or other
; NAME/KEY: modified_base
; LOCATION: (151)
; OTHER INFORMATION: a, t, c, g, unknown or other
; NAME/KEY: modified_base
; LOCATION: (311)
; OTHER INFORMATION: a, t, c, g, unknown or other
; NAME/KEY: modified_base
; LOCATION: (322)
; OTHER INFORMATION: a, t, c, g, unknown or other
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Job time : 430.232 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 07:25:32 ; Search time 101.11 Seconds
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1386.561 Million cell updates/sec

Title: US-09-977-579A-4_COPY_1_375

Perfect score: 375
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
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5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
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8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:
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10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	375	100.0	1261	6	US-10-374-954-8
C 2	44.8	11.9	169495	7	US-11-121-086-61
3	40.2	10.7	2838	6	US-10-770-726-27
C 4	39	10.4	1931	6	US-10-750-185-46989
5	37.8	10.1	160226	7	US-11-121-086-29
6	35.4	9.4	2793	6	US-10-750-185-32170
7	35.4	9.4	246960	7	US-11-121-086-8
C 8	35	9.3	5679	7	US-11-075-185-36
C 9	35	9.3	78869	7	US-11-075-185-1
10	34.8	9.3	1557	6	US-10-996-217A-6
11	34.8	9.3	2820	6	US-10-750-185-46988
C 12	34.8	9.3	161874	7	US-11-121-086-75
13	34.4	9.2	2375	7	US-11-108-528-63
14	34	9.1	1830	7	US-11-064-774A-120
C 15	33.8	9.0	150038	7	US-11-121-086-23
C 16	33.6	9.0	150468	7	US-11-112-908-56
C 17	33.6	9.0	193789	7	US-11-112-908-55
C 18	33.4	8.9	708	7	US-11-075-185-59
C 19	33.2	8.9	1386	6	US-10-509-464-3
20	33.2	8.9	5301	7	US-11-075-185-40
21	33.2	8.9	78869	7	US-11-075-185-1
C 22	33	8.8	191684	7	US-11-121-086-2
C 23	32.8	8.7	600	6	US-10-750-185-23

24	32.8	8.7	9710	6	US-10-655-872-1	Sequence 1, Appli
25	32.6	8.7	1975	6	US-10-750-185-56875	Sequence 56875, A
C 26	32.4	8.6	1777	6	US-10-750-185-60816	Sequence 60816, A
27	32.4	8.6	2786	7	US-10-750-185-29861	Sequence 29861, A
C 28	32.4	8.6	189252	7	US-11-121-086-54	Sequence 54, Appl
C 29	32.2	8.6	1434	7	US-11-075-185-57	Sequence 57, Appl
30	32.2	8.6	1723	7	US-11-051-568-28	Sequence 28, Appl
31	32.2	8.6	4854	6	US-10-821-234-103	Sequence 103, App
C 32	32.2	8.6	14172	7	US-11-075-185-2	Sequence 2, Appli
C 33	32.2	8.6	191091	7	US-11-121-086-60	Sequence 60, Appl
34	32	8.5	168516	7	US-11-121-086-3	Sequence 3, Appli
35	31.8	8.5	1196	6	US-10-750-185-47546	Sequence 47546, A
C 36	31.8	8.5	11070	7	US-11-075-185-34	Sequence 34, Appl
37	31.8	8.5	17162	7	US-11-112-908-38	Sequence 38, Appl
C 38	31.6	8.4	2276	6	US-10-131-826A-9	Sequence 9, Appli
C 39	31.6	8.4	180654	7	US-11-121-086-58	Sequence 58, Appl
C 40	31.6	8.4	235033	7	US-11-157-389-1	Sequence 1, Appli
C 41	31.6	8.4	237326	7	US-11-157-389-2	Sequence 2, Appli
C 42	31.4	8.4	168516	7	US-11-121-086-3	Sequence 3, Appli
C 43	31.4	8.4	171936	6	US-10-933-025-24	Sequence 24, Appl
C 44	31.4	8.4	172147	7	US-11-112-908-22	Sequence 22, Appl
C 45	31.4	8.4	188682	7	US-11-112-908-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-10-374-954-8
; Sequence 8, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (376)..(1023)
US-10-374-954-8

Query Match 100.0%; Score 375; DB 6; Length 1261;

Best Local Similarity 100.0%; Pred. No. 8.5e-80;

Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCCTCCCTTCGAGCTGAGCTTACCTCGGCGGCAACAGCAGGAGCGGCGGCGGCTGG 60
Db	1	CCCTCCCTTCGAGCTGAGCTTACCTCGGCGGCAACAGCAGGAGCGGCGGCGGCTGG 60
Qy	61	AAGCTGGAGTTCGCGGGTGGCGGAGGAGCTGTCCGTGGTGTCTGAGCGCCGCGAGA 120
Db	61	AAGCTGGAGTTCGCGGGTGGCGGAGGAGCTGTCCGTGGTGTCTGAGCGCCGCGAGA 120
Qy	121	GCGGCGCGGAGCGGCTGATCGGCTCCCTCAAACTGGGAGGTCCAGTGGGGTTCGCTTAG 180
Db	121	GCGGCGCGGAGCGGCTGATCGGCTCCCTCAAACTGGGAGGTCCAGTGGGGTTCGCTTAG 180
Qy	181	GGCCCAAGCCCCACCCCGCTCAAAAGCTCCAGGGCTCCCGAGCCACCGGTGCTCG 240
Db	181	GGCCCAAGCCCCACCCCGCTCCAAAAGTCCCGAGGGCTCCCGAGCCACCGGTGCTCG 240

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Qy 241 GCCCTTCTCTCGGTGAGAAAGTCGCCCTCGGGGCGAGTTGTTCCCAAGGGTTTCTCTCG 300
Db 241 GCCCTTCTCTCGGTGAGAAAGTCGCCCTCGGGGCGAGTTGTTCCCAAGGGTTTCTCTCG 300
Qy 301 AAAGAAATCTGAGAGGGCGCAGTCTTACCGAGGGAATCTCTGTGTAGCCTTGGAGC 360
Db 301 AAAGAAATCTGAGAGGGCGCAGTCTTACCGAGGGAATCTCTGTGTAGCCTTGGAGC 360
Qy 361 CGCCAGCCCCAGAAG 375
Db 361 CGCCAGCCCCAGAAG 375

RESULT 2
US-11-121-086-61/c
; Sequence 61, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-0000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 169495
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (70072)..(70171)
; OTHER INFORMATION: a, c, g, t, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (139457)..(157244)
; OTHER INFORMATION: a, c, g, t, unknown or other
;
US-11-121-086-61
Query Match 11.9%; Score 44.8; DB 7; Length 169495;
Best Local Similarity 56.7%; Pred. No. 0.02;
Matches 102; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

Qy 74 GGGTGGCGGGAGGCGACTGTCGTGTGTCAGCGCGCGGAGAGCGGGCGCGAGC 133
Db 45491 GGGAGGGCGGGTAGGGACCTTTACAGAGCCAGGAGGGCTTTCGGGGCGGTGGGGCGCGC 45432
Qy 134 GCCTGATCGGTCCCTCGAACTGGGGAGGTCAGTGGGTGCG-CTTAGGGCCCAAGGCC 192
Db 45431 TCGGAGCGGAGCGCGCGCTCGACGCGGTGCGTGGCGGCGAGTGTATGCAGACGGCGC 45372
Qy 193 CCACCGCGCTCCAAAAGTCCCGAGGCGCTCCCGAGGACCGGTGCTGGCGCCTTCCCTTCG 252
Db 45371 CGGGCCCGAACCCGAGCCCCCGGGGCTCCCGACCGCGGCTCCCGCGCTCCCGCGC 45312

RESULT 3
US-10-770-726-27
; Sequence 27, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-27

Query Match 10.7%; Score 40.2; DB 6; Length 2838;
Best Local Similarity 49.8%; Pred. No. 0.25;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Qy 23 ACCCTGGGCGCAACGAGCGAGCGGGGCGCAGTGGAGTTCGAGTTCGGGGTGGGC 82
Db 577 ACCACGGCCAGAGGGGCGCCAGGGAAGGACGAGCGCGGTTCGCCGGTTCACAGC 636
Qy 83 GGGGAGGCGACTGTCGTGTGTCGTAGCGCGCGGCGAGAGCGGGCGCGGCGGTGATCG 142
Db 637 GAGCGGGTGGCGGAGTGTGTGACGCGAGCGGGCGGGCCAGAGAGAGCCCAAGTCT 696
Qy 143 GCTCCCTCGAACTGGGAGGTCCAGTGGGTGCGCTTAGGGCCCAAGCCCGCGGCT 202
Db 697 TCCAGGGAGGGCTCAGGGGTCCCCAGGAGTCTCTCCGGGACAAACGCCCTCTCCGGG 756
Qy 203 CAAAAGCTCCGAGGGCTCCCCCAG 227
Db 757 CCTGATGTCGGCACCCCCCAGCCTG 781

RESULT 4
US-10-750-185-46989
; Sequence 46989, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46989
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Bovine
19866880829104
US-10-750-185-46989

Query Match 10.4%; Score 39; DB 6; Length 1931;
Best Local Similarity 52.8%; Pred. No. 0.48;
Matches 84; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 54 CGAGTGAAGCTGAGTTCGGGGTGGGCGGAGGAGCACTGTCGTGTGTCGAGCGCC 113
Db 1745 CGAGAGGCGCTGTGAGTCAACACCTTCATGGGGGCGACGCTGCCACCGCGCTGTGCA 1804
Qy 114 GCGAGAGCGGGCGGAGGCGGTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGT 173
Db 1805 AAGAGGAACAGGGTCAGAGCTGGAGATGGGATCACAGGGCGCCTAGGTACAGTAGGCC 1864
Qy 174 CGCTTAGGGCCCAAGCGCCCGCGCTCCAAAAGCTC 212
Db 1865 CTCTGAGACCTGGAGAGCGCTCCCGGCTTCATACCCCC 1903

RESULT 5
US-11-121-086-29/c
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Qy 231 CCGGTGCTCGGCC 244
      |||
Db 1533 CAGAAGCAGCCCC 1546
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RESULT 12
US-11-121-086-75/c
; Sequence 75, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75
; LENGTH: 161874
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-75

Query Match 9.3%; Score 34.8; DB 7; Length 161874;
Best Local Similarity 60.6%; Pred. No. 4.3;
Matches 57; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 45 GCAGGGCGCGAGTGGAAAGCTGGAGTTCCGGGGTGGCGGGGAGGCGCACTGTCCGTGGTG 104
      |||
Db 77243 GCGGGGCGGGGTGGGAACCTCGAAACCTGCGAGGCGCGGAGCGGCTGCAAGGGCG 77184
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Qy 105 CTGAGCGCCCGCGAGAGCGGGCGCGGAGCGGTG 138
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Db 77183 GGGAAAGCGGGAGCCGCGCAGCGAGGAGGGGGCG 77150
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RESULT 13
US-11-108-528-63
; Sequence 63, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Glenn
; APPLICANT: Marvin, Martha
; APPLICANT: Li, Dean Y.
; APPLICANT: Wang, Elizabeth
; APPLICANT: Chen, C. M. Amy
; APPLICANT: Shamah, Steven M.
; TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: HYDR-POL-041
; CURRENT APPLICATION NUMBER: US/11/108,528
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,137
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/598,368
; PRIOR FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 2375
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-108-528-63

Query Match          9.2%; Score 34.4; DB 7; Length 2375;
Best Local Similarity 45.5%; Pred. No. 5.7;
Matches 122; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

QY      88  GGGCACTGTCGGTGGCTGAGCGCGCGGAGAGCGGCGGCTGATCGGCTCC 147

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REFUGAT, NIELSEN, KARSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

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; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 150038
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-23

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	Query Match	9.0%	Score 33.8	DB 7	Length 150038
	Best Local Similarity	54.4%	Pred. No. 7.4		
	Matches 68	Conservative 0	Mismatches 57	Indels 0	Gaps 0
Qy	48	GGGGCCGAGTGAAGCTGGAGTTCGGGAGTGGCGGGAGGCGGACTGTCGTTGCTGCTG	107		
Db	26692	GTGGTGGAGTGGCGGTGGAGATGCGCGGTGAGGTGGAGTGGTGGAGATGGCG	26633		
Qy	108	AGGCCGCGGAGAGCGGGCGCGGAGCGGTGATCGGCTCCCTCGAACTGGGAGGTCGAG	167		
Db	26632	CGTGGTGGAGGTGGCGGCGGTGGCAGAGGTGTTGGGTGGAGGTGTTGAGTGGAGG	26573		
Qy	168	TGGGG	172		
Db	26572	TGGCG	26568		

Search completed: December 13, 2005, 14:42:57
Job time : 106.11 secs

Db 251 CACCAAGACCTGCAGGATCTGTCTATCTTCATCACCAATGTCCATACCAACCACTCGG 310
Qy 348 CCTCTACACCTGCATGTCCGGAGTTTGAGTTTGAGGGCGATCGGCCCTTTGTCAA 407
Db 311 CGACTACGAGTGCCACGCTCTACCGCTCTCTTCTTCGAAAACACTACGAGCACAACCCAG 370
Qy 408 GACGACGGGCTGATCCCCCTCAAGAGTCACCGAGGAGCTGGAGAGGACTTCACCTCTGT 467
Db 371 CGTCGTCAGAAGATCCACATTTAGGTAGTGACAAAGCCACAGACATGGCATCCAT 430
Qy 468 GGTCTCAGAAATCATGATGATACCTTCTGGTCTTCTCTCACTCCCTGTGGCTGCTCATCGA 527
Db 431 CGTGTCTGAGATCATGATGTGTCTCATTTGTGTGTGACCATATGGCTCGTGGCAGA 490
Qy 528 GATGATATTTGCTACAGAAAGGTTCTCAAAAGCCGAAGAG---CGAGCCCAAGAAACGC 584
Db 491 GATGATTTTACTGCTACAGAAGATCGCTGCGCCCAACGAGACTGCTGCACAGGAGATGC 550
Qy 585 GTCTGACTACCTTGCCATCCCATCTGAGAACAAAGGAGAACTCTCGGG 631
Db 551 CTCGGAATACCTGGCCATCACCTCTGAAGCAAGAGAACTGCACGG 597

RESULT 2

US-09-949-016-14111
; Sequence 14111, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14111
; LENGTH: 11174
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(11174)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14111

Query Match 7.9%; Score 51; DB 3; Length 11174;
Best Local Similarity 58.1%; Pred. No. 0.001;
Matches 90; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
Qy 66 CTTCCCTGTGTGTGGAAGTGCCCTCGAGACGGAGCCGTGACGGGCAACCCCATGAA 125
Db 2011 CTGCGGGGGCTGCGTGGAGTGGACTCGGAGACCGAGCCGTGTATGGGATGACCTTCAA 2070
Qy 126 GCTGGCTGTCATCTCCTCATGAAGAGAGAGGTGGAGGCCACACGGTGGTGAATG 185
Db 2071 AATCTTTGATCTCTCTCAAGCCGCGCAGGAGACCAACCGTGTGACCTTCACCGAGTG 2130
Qy 186 GTTCTACAGGCCCGGCGGTAAAGATTTCTTTA 220
Db 2131 GACCTTCGCCCAAGAGGGCACTGAGGAGTTTGTCA 2165

RESULT 3

US-09-949-016-13053
; Sequence 13053, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13053
; LENGTH: 30337
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(30337)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13053

Query Match 7.5%; Score 48.6; DB 3; Length 30337;
Best Local Similarity 63.0%; Pred. No. 0.0068;
Matches 75; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Qy 454 GACTTCACCTCTGTGGTCTCAGAAATCATGATGTACATCTTCTGGTCTTCTCACCCTG 513
Db 620 GACATGCGATCCATCGGTCTGAGATCATGATGTATGTCTCATTTGGTGTGACCAT 679
Qy 514 TGGCTGCTCATCGAGATGATATTTGCTACAGAAAGTCTCAAAAGCCGAAGGCGAGC 572
Db 680 TGGCTGCTGCGAGAGATGATTACTGTACAAGAAGATCGTCCGCCACCGAGACTGC 738

RESULT 4

US-09-023-587A-5
; Sequence 5, Application US/09023587A
; Patent No. 6653530
; GENERAL INFORMATION:
; APPLICANT: Shewmaker, Christine K.
; APPLICANT: Bhat, Ganesh B.
; APPLICANT: Venkatramesh, Mylavaram
; APPLICANT: Rangwala, Shaikat H.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Boddupalli, Sekhar S.
; TITLE OF INVENTION: Methods for Producing Carotenoid Compounds, Tocopherol Compounds,
; SPECIALTY OILS IN PLANT SEEDS
; FILE REFERENCE: 16516.122
; CURRENT APPLICATION NUMBER: US/09/023,587A
; CURRENT FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1645
; TYPE: DNA
; ORGANISM: Zea mays
US-09-023-587A-5

Query Match 7.0%; Score 45.4; DB 3; Length 1645;
Best Local Similarity 46.2%; Pred. No. 0.018;
Matches 151; Conservative 0; Mismatches 176; Indels 0; Gaps 0;
Qy 54 GGTCAAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGAGACGCGAGGCCGTGCGAGG 113
Db 349 GGTGCTCAACGGCTCTTCTTAAGGTACGAGCGCCCAAGAGCGCCGAACGGCTGTAGT 408
Qy 114 CAACCCCATGAAGTGGCGCTGTCATCTCTCATGAAGAGAGAGAGGTGGAGGCCACAC 173
Db 409 GGTGCACTACAAACCACTACGACGCGCAGCAACGGCAAGGTCTCGCGCGGAGAGCGGT 468


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RESULT 8
US-09-540-1203
; Sequence 1203, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1203
; LENGTH: 23738
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-540-1203

Query Match      6.5%; Score 42.4; DB 3; Length 23738;
Best Local Similarity 51.6%; Pred. No. 0.31;
Matches 97; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 87 GCCTCGAGAGGAGGCGCGTGGAGGCAACCCCATGAGCTGCGCTGCATCTCTGCAT 146
DB 4191 GCGCAGGATGATGGCGGCGGCCATCCGTTTCAAGACGCGTGCAAGCCGCGTGCAG 4250

QY 147 GAAGAGAGAGGAGTGGAGGCCACACACGCTGGTGGATGTTCTACAGGCCGAGGGCGG 206
DB 4251 GAAGCGGCGGAGGATGCGGACACGCTGGCGTGGAACCGCTTCCGACCACTGCTGT 4310

QY 207 TAAAGATTTCCTTATTTACGAGTATCGGAATGGCCACAGGAGGTGGAGAGCCCTTTCA 266
DB 4311 GGGTGAAGCGCTCCGCTACGAGGATCTGCGGGAATCCAGCTCGACAGCGCGGTGCA 4370

QY 267 GGGCGGCC 274
DB 4371 GCTCGGCC 4378

RESULT 9
US-09-489-039A-3591
; Sequence 3591, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3591
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3591

Query Match      6.4%; Score 41.6; DB 3; Length 696;
Best Local Similarity 48.3%; Pred. No. 0.14;
Matches 116; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 83 AAGTCCCTCGAGACGAGGCGGTGGAGGCAACCCCATGAAGCTGCGCTGCATCTCTCT 142
DB 92 AGGCGCGGACGCTCGCGAGCGGTGCTGGGAAGCTGCCGAAGCGCGGTATGCCGACT 151
QY 143 GCATGAAGAGAGGAGGTGGAGGCCACACGCTGTTGGAATGTTCTACAGGCCCGGAGG 202

Db 152 ACCTGCGGTTCAACGACGTTTGAACGTTACCCCGCTGGATCAGGCGATTCGCTGTGGTTCC 211
QY 203 GCGTAAAGATTTCCTTATTTACGAGTATCGGAATGCCACAGGAGGTGAGAGCCCT 262
DB 212 CCGGGCCGAATCTCTTTTACCGGGGAAGATGTCTTGAGCTGCAGGGCCACGGGCGCCGG 271
QY 263 TTCAGGGGCGCTGCACTGAGTGAATGGCAGCAAGGACCTGCAGGAGGTGTCCATCACTGTGC 322
DB 272 TCATTCTGACCTGCTGCTTAAACGATATTCTGACCCCTGCCGGGCTGGCATCCGAGGC 331

RESULT 10
US-09-902-540-3929
; Sequence 3929, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3929
; LENGTH: 2943
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3929

Query Match      6.3%; Score 40.6; DB 3; Length 2943;
Best Local Similarity 48.9%; Pred. No. 0.45;
Matches 109; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 85 GTGCGCTCGAGAGGAGCGCGTGCAGGCAACCCCATGAAGCTGCGCTGCATCTCTGC 144
DB 1831 GTGCTGGAAGAGGTGGAGCGCGCGCTGCGGAGTGTGCGCTGATGCCGCGAGGCCGCG 1890

QY 145 ATGAAGAGAGGAGGTGGAGGCCACCAACGCTGTGGAATGTTCTACAGGCCCGAGGCG 204
DB 1891 ATGCGCTACGCGCAGGAGCTGAAGCCCGCGGTGAGCGCGCGCGCCAGGTGAAGGC 1950

QY 205 GGTAAGATTTCCTTATTTACGAGTATCGGAATGGCCACAGGAGGTGGAGAGCCCTTT 264
DB 1951 GCCTATGACCGCTCTCTGGACGCTTCACCGGCCGCGGTGAGCGCTGTGTG 2010

QY 265 CAGGGGCGCTGCACTGGAATGGCAGCAAGGACCTGCAGGACG 307
DB 2011 AAGCGCGCCAGGAGCGCATGGGCGATCGAGCGCGAGGAGG 2053

RESULT 11
US-09-902-540-1194
; Sequence 1194, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1194
; LENGTH: 21295
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; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1194

Query Match      6.3%; Score 40.6; DB 3; Length 21295;
Best Local Similarity 48.9%; Pred. No. 0.94; 114; Indels 0; Gaps 0;
Matches 109; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

Qy 85 GTGCCCTCGGAGACGAGCGCGTGCAGGGCAACCCCATGAAGCTGCGGTGCATCTCTGTC 144
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2609 GTGCTGGAAGAGGTGGAGGCGCGCTGCGCAGCTGCGCTGATGCCGCGGAGGCGCGC 2668

Qy 145 ATGAAGAGAGAGGAGGTGGAGGCCACACGCGTGTGTGAATGTTCTACAGGCCCGAGGGC 204
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2669 ATGCGCTACGCGCAGGAGCTGAAGCGCCGCGCTGGAGCGCGCGCCGACAGGTGAAGCGC 2728

Qy 205 GGTAAAGATTTCCTTAATTACAGATATCGGAATGCCACACAGGAGGTGGAGCCCTTT 264
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2729 GCCTATGACCTCGCTCTGGACGTGCGCAGCTTCGACCGCGCCGCGGTGGAGCGCTGGTG 2788

Qy 265 CAGGGCGCCCTGCAGTGAATGGCAGCAAGGACCTGCAGGACG 307
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2789 AAGCGGCCACGAGGCGCATCGAGCCGACGAGGAGG 2831

RESULT 12
US-09-902-540-7877
; Sequence 7877, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7877
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-7877

Query Match      6.2%; Score 40.4; DB 3; Length 1533;
Best Local Similarity 47.9%; Pred. No. 0.4;
Matches 116; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

Qy 232 CGGAATGCCACGAGGAGTGAGAGCCCTTTTCAGGGCGCCCTGCAGTGAATGGCAGC 291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 310 CGGGATGCCCGAGCAGTTGAGTCTCCGAGGGAGGGCTCGTCTCGGGATGGGGAC 369

Qy 292 AAGGACCTGCAGGAGCTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTGGCTC 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 370 ACGGAGCTGCAGGACCTGTGTGGCGCGGTACAGGTGACGGCGGCTGCTCAGTGGGC 429

Qy 352 TACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAAGCGCATCGGCCCTTTGTGAAGACG 411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 430 TTCAGGACGACCCATCGCGTGGGCTCGTGAAGGGGGCGCTGGCGAAGCTGGGCATCAC 489

Qy 412 ACGGGCTGATCCCTTAAGAGTACCGAGAGGCTGGAGAGGACTTACCTCTGTGGTC 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 490 GTGCTGGTCGCGCTGCTCGTCTTACCGCGCGGCGCTTCTGGTCCAGCGCGCCATCGTG 549

Qy 472 TC 473
    ||
Db 550 TC 551

RESULT 13
US-09-902-540-789
; Sequence 789, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 789
; LENGTH: 5228
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-789

Query Match      6.2%; Score 40.4; DB 3; Length 5228;
Best Local Similarity 47.9%; Pred. No. 0.64;
Matches 116; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

Qy 232 CGGAATGCCACGAGGAGTGAGAGCCCTTTTCAGGGCGCCCTGCAGTGAATGGCAGC 291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3057 CGGGATGCCCGAGCAGTTGAGTCTCCGAGGGAGGGCTCGTCTCGGGATGGGGAC 3116

Qy 292 AAGGACCTGCAGGAGCTGTCCATCACTGTGCTCACTCACTCACTCACTCACTCACTCA 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3117 ACGGAGCTGCAGGACCTGTGGCGCGGTACCAAGGTACGCCGCGCTGGTCCACGTGGGC 3176

Qy 352 TACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAAGCGCATCGGCCCTTTGTGAAGACG 411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3177 TTCAGCGCACCATGTGGCTGCTGGAAGGGGCGCTGGCGAAGCTGGGCATCAC 3236

Qy 412 ACGCGGCTGATCCCTTAAGAGTACCGAGAGGCTGGAGAGGACTTCACTCTGTGGTC 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3237 GTGCTGGTCGCGCTGCTCGTCTTACCGCGCGGCGCTTCTGCTGGTCAGCGCGGCATCGTG 3296

Qy 472 TC 473
    ||
Db 3297 TC 3298

RESULT 14
US-09-902-540-3806
; Sequence 3806, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3806
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3806

Query Match      6.0%; Score 39.2; DB 3; Length 732;
Best Local Similarity 49.5%; Pred. No. 0.66;
Matches 101; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Qy 297 CTGCGAGGACGTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTGGCCTCTACAC 356
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Db      480 CCTGGAGGACATGTCGGACGACGTGAAGATCGCGCGCTCAAGGCGCTGGGCGTCTTCAA 539
Qy      357 CTGCAATGTGTCCTGGGAGATTTGAGTTGAGGCGCATCGGCCCTTTGTGAGAGAGAGCGCG 416
Db      540 GTACGAGCGGCGCGCGAGCCCATGCTGAAGCTCTCACCGCCGACGAGAGCGGCTCGCCG 599
Qy      417 GCTGATCCCCCTAAGATGTCACGAGGAGGCTGGAGAGACTTTCACCTCTGTGGTCTCAGA 476
Db      600 GGTGCAGACGTCCGTACTCAGCGCGCTGCGGGAAGGTGGCTTCTCCGTGAGGGCTACCG 659
Qy      477 AATCATGATGTACATCTCTTCTGGT 500
Db      660 GGAGAGGTGGAGCGCGTGTCTGGT 683
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RESULT 15
US-09-774-528-120
; Sequence 120, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL genes Version 2.0
; SEQ ID NO 120
; LENGTH: 6202
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49)...(4890)
US-09-774-528-120
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Query Match      6.0%; Score 39.2; DB 3; Length 6202;
Best Local Similarity 47.2%; Pred. No. 1.4;
Matches 119; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

Qy      93 GGAGACGAGGCGGTGACGAGCAACCCCATGAAGCTGCGTGCATCTCTCGATGAAAGAG 152
Db      2418 GCACAAGGAGTCTGGGGAGAGCACGGTGACATGCTGAAGCGCAAGCGGAGCTGGAGGA 2477
Qy      153 AGAGAGGTGGAGGCGACACCGGTGGTGAATGGTTCTACAGGCCCGGAGGGCGGTAAAGA 212
Db      2478 GCGGAGGAAGGTCTTGACCACTGACGAGAGGCGCTGCAGCAGGAGCAGAGGACAAACGC 2537
Qy      213 TTTCTTTATTACAGATATCGGAATGCGCAACAGAGGTGGAGAGCCCTTTTCAGGGCGG 272
Db      2538 CCTGCCATGGCGAGAACCAAGAGGCTGCGGGCGAGCTGGACAGGGTCAATTTCTCTGCA 2597
Qy      273 CCTGAGTGGATGCGCAGCAGGACCTGCAGAGCTGTCCATCACTGTGCTCAACGTCAC 332
Db      2598 CCACCAGCTGAAGGGGGAGTACGAGGAGTGCACGCCCCACCAAGGAGCTGAACACCTC 2657
Qy      333 TCTGAACGACTC 344
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Db      2658 ACTGAACACACGC 2669

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OM nucleic - nucleic search, using sw model

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(without alignments)
7241.448 Million cell updates/sec

Title: US-09-977-579A-4_COPY_376_1023

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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- Published Applications NA_Main:
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 - 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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 - 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	646.4	99.8	1261	9	US-10-482-834A-22
3	536.6	82.8	2220	3	US-03-977-579-3
4	536.6	82.8	2632	5	US-10-029-191-22
5	536.6	82.8	3108	9	US-10-029-191-1
6	534.8	82.5	1195	9	US-10-450-763-22568
7	534.6	82.5	645	5	US-10-029-191-21
8	392.6	60.6	3531	9	US-10-450-763-22567
9	362	55.9	600	10	US-11-060-756-2816
10	362	55.9	600	10	US-11-060-756-2817
11	362	55.9	600	10	US-11-060-756-7088
12	362	55.9	600	10	US-11-060-756-7089
13	229.2	35.4	545	4	US-09-925-065A-774904
14	224.4	34.6	621	9	US-10-450-763-22566
15	148.2	22.9	657	5	US-10-029-191-23
16	143.8	22.2	1275	10	US-11-060-756-3901
17	143.8	22.2	1275	8	US-11-060-756-8173
18	143.8	22.2	1335	8	US-10-723-860-2247
19	142.2	21.9	1414	8	US-10-477-272-1
20	142.2	21.9	1414	9	US-10-482-834A-11
21	142.2	21.9	1414	9	US-10-482-834A-12
22	141	21.8	407	7	US-10-276-774-718
23	138.6	21.4	1490	3	US-09-917-800A-1654

24	81.4	12.6	807	6	US-10-401-916-12	Sequence 12, Appl
25	81.4	12.6	974	6	US-10-401-916-13	Sequence 13, Appl
26	55	8.5	651	4	US-09-925-065A-513767	Sequence 513767,
27	55	8.5	651	4	US-09-925-065A-513768	Sequence 513768,
28	55	8.5	651	4	US-09-925-065A-513769	Sequence 513769,
29	51	7.9	502	4	US-09-925-065A-807996	Sequence 807996,
30	49	7.6	243	6	US-10-029-386-16214	Sequence 16214, A
31	49	7.6	569	6	US-10-029-386-2514	Sequence 2514, Ap
32	48.6	7.5	3583	8	US-10-723-860-6471	Sequence 6471, Ap
33	45.4	7.0	876	7	US-10-767-701-10747	Sequence 10747, A
34	45.4	7.0	1645	9	US-10-647-517-29	Sequence 29, Appl
35	45.2	7.0	954	8	US-10-425-115-100998	Sequence 100998,
36	45	6.9	495	4	US-09-925-065A-778585	Sequence 778585,
37	45	6.9	496	4	US-09-925-065A-807954	Sequence 807954, A
38	44.8	6.9	921	6	US-10-369-493-43050	Sequence 43050, A
39	44	6.8	53	9	US-10-491-192-5	Sequence 5, Appli
40	44	6.8	60	9	US-10-491-192-6	Sequence 6, Appli
41	43.8	6.8	1434	6	US-10-259-194A-622	Sequence 622, App
42	43.8	6.8	1720	7	US-10-425-114-19213	Sequence 19213, A
43	43.8	6.8	1764	7	US-10-425-114-15538	Sequence 15538, A
44	43.8	6.8	1794	7	US-10-425-114-25057	Sequence 25057, A
45	43.8	6.8	2029	8	US-10-425-115-15884	Sequence 15884, A

ALIGNMENTS

RESULT 1
US-09-977-579-4
; Sequence 4, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
; TITLE OF INVENTION: channel
; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977,579
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-977-579-4

Query Match	100.0%	Score 648;	DB 3;	Length 1261;
Best Local Similarity	100.0%	Pred. No. 1.4e-200;	Mismatches 0;	Indels 0;
Matches 648;	Conservative 0;			Gaps 0;
Qy	1	ATGCCTCCCTCAATAGATTGTTTCCCTCGCTCTCTCGTGTATCTACTGGTCACT	60	
Db	376	ATGCCTCCCTCAATAGATTGTTTCCCTCGCTCTCTCGTGTATCTACTGGTCACT	435	
Qy	61	GTCTGCTTCCCTGTGTGTGGAAAGTCCCTCGAGACGGAGCCGTGACGGGCAACCCC	120	
Db	436	GTCTGCTTCCCTGTGTGTGGAAAGTCCCTCGAGACGGAGCCGTGACGGGCAACCCC	495	
Qy	121	ATGAAGTCGGCTGCATCTCTGCATCAAGAGAGAGAGTGGAGCCACCACCGTGGTG	180	
Db	496	ATGAAGTCGGCTGCATCTCTGCATCAAGAGAGAGAGTGGAGCCACCACCGTGGTG	555	
Qy	181	GAATGGTTTCTACAGCCCGGCGGTAAAGATTTCTTATTACAGATTCGGAATGGC	240	
Db	556	GAATGGTTTCTACAGCCCGGCGGTAAAGATTTCTTATTACAGATTCGGAATGGC	615	
Qy	241	CACGAGAGTGGAGAGCCCTTTACGGGCGCTGAGTGGAAATGGCAGCAAGACTG	300	

Db 616 CACCAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTTCAGTGAATGGCAGCAAGGACCTG 675
Qy 301 CAGGACGTGTCACACACTGCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGC 360
Db 676 CAGGACGTGTCACACACTGCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGC 735
Qy 361 AATGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 420
Db 736 AATGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 795
Qy 421 ATCCCCCTAAGAGTCAACGAGAGGCTGGAGAGACTTCACTCTGTGGTCTCAGAAATC 480
Db 796 ATCCCCCTAAGAGTCAACGAGAGGCTGGAGAGACTTCACTCTGTGGTCTCAGAAATC 855
Qy 481 ATGATGTACATCCTTCTGGTCTTCTCACTACCTGTGGCTGCTCATCGAGATGATATATGC 540
Db 856 ATGATGTACATCCTTCTGGTCTTCTCACTACCTGTGGCTGCTCATCGAGATGATATATGC 915
Qy 541 TACAGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGGGTCTGACTACCTTGGC 600
Db 916 TACAGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGGGTCTGACTACCTTGGC 975
Qy 601 ATCCCATCTGAGAACCAAGGAGAACTCTCGGTACCAAGTGGAGGAATAG 648
Db 976 ATCCCATCTGAGAACCAAGGAGAACTCTCGGTACCAAGTGGAGGAATAG 1023

RESULT 2

US-10-482-834A-22

; Sequence 22, Application US/10482834A

; Publication No. US20050074764A1

; GENERAL INFORMATION:

; APPLICANT: Mulley, John Charles

; APPLICANT: Harkin, Louise Anne

; APPLICANT: Dibbens, Michelle

; APPLICANT: Wallace, Robyn

; APPLICANT: Phillips, Hillary Ann

; APPLICANT: Heron, Sara Elizabeth

; APPLICANT: Berkovic, Samuel Frank

; APPLICANT: Scheffer, Ingrid Eileen

; APPLICANT: Biomedics Limited

; TITLE OF INVENTION: MUTATIONS IN ION CHANNELS

; FILE REFERENCE: 1386/17

; CURRENT APPLICATION NUMBER: US/10/482,834A

; CURRENT FILING DATE: 2004-01-02

; NUMBER OF SEQ ID NOS: 173

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 22

; LENGTH: 1261

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-482-834A-22

Query Match 99.8%; Score 646.4; DB 9; Length 1261;
Best Local Similarity 99.8%; Pred. No. 4.7e-200;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTGCTTATCTACTGGGTCAGT 60
Db 376 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTGCTTATCTACTGGGTCAGT 435

Qy 61 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGGAGAGGAGGCGGTGAGGCGCAACCCC 120
Db 436 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGGAGAGGAGGCGGTGAGGCGCAACCCC 495

Qy 121 ATGAAGCTGCGTGCATCTCTCTGCATGAAGAGAGGAGGTGGAGGCCACACCGTGGTG 180
Db 496 ATGAAGCTGCGTGCATCTCTCTGCATGAAGAGAGGAGGTGGAGGCCACACCGTGGTG 555

Qy 181 GAATGGTTCTACAGGCCCGGCGGTAAAGATTTCTTATTTACGAGTATCGGAATGGC 240
Db 556 GAATGGTTCTACAGGCCCGGCGGTAAAGATTTCTTATTTACGAGTATCGGAATGGC 615

Qy 241 CACCAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTTCAGTGAATGGCAGCAAGGACCTG 300
Db 616 CACCAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTTCAGTGAATGGCAGCAAGGACCTG 675
Qy 301 CAGGACGTGTCACACACTGCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGC 360
Db 676 CAGGACGTGTCACACACTGCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGC 735
Qy 361 AATGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 420
Db 736 AATGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 795
Qy 421 ATCCCCCTAAGAGTCAACGAGAGGCTGGAGAGACTTCACTCTGTGGTCTCAGAAATC 480
Db 796 ATCCCCCTAAGAGTCACTGAGGAGGCTGGAGAGACTTCACTCTGTGGTCTCAGAAATC 855
Qy 481 ATGATGTACATCCTTCTGGTCTTCTCACTACCTGTGGCTGCTCATCGAGATGATATATGC 540
Db 856 ATGATGTACATCCTTCTGGTCTTCTCACTACCTGTGGCTGCTCATCGAGATGATATATGC 915
Qy 541 TACAGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGGGTCTGACTACCTTGGC 600
Db 916 TACAGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGGGTCTGACTACCTTGGC 975
Qy 601 ATCCCATCTGAGAACCAAGGAGAACTCTCGGTACCAAGTGGAGGAATAG 648
Db 976 ATCCCATCTGAGAACCAAGGAGAACTCTCGGTACCAAGTGGAGGAATAG 1023

RESULT 3

US-09-977-579-3

; Sequence 3, Application US/09977579

; Publication No. US20040248240A1

; GENERAL INFORMATION:

; APPLICANT: Cambridge University Technical Services

; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod

; TITLE OF INVENTION: channel

; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t

; FILE REFERENCE: 674558-2001

; CURRENT APPLICATION NUMBER: US/09/977,579

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: PCT/EP00/01783

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60,129,473

; PRIOR FILING DATE: 2000-02-24

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 2220

; TYPE: DNA

; ORGANISM: rat

US-09-977-579-3

Query Match 82.8%; Score 536.6; DB 3; Length 2220;
Best Local Similarity 89.3%; Pred. No. 4.2e-164;
Matches 578; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 1 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTGCTTATCTACTGGGTCAGT 60
Db 363 ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGTCTCATCTACTGGGTCAGA 422

Qy 61 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGGAGAGGAGGCGGTGAGGCGCAACCCC 120
Db 423 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGGAGAGGAGGCGGTGAGGCGCAATCCC 482

Qy 121 ATGAAGCTGCGTGCATCTCTCTGCATGAAGAGAGGAGGTGGAGGCCACACCGTGGTG 180
Db 483 ATGAAGCTGAGTGCATCTCTCTGCATGAAGAGGAGGAGGTGGAGGCCACCACTGTGGTG 542

Qy 181 GAATGGTTCTACAGGCCCGGCGGTAAAGATTTCTTATTTACGAGTATCGGAATGGC 240
Db 543 GAGTGGTTCTACAGGCCCGTAAAGATTTCTTATATATGAGTATCGGAATGGC 602

QY 241 CACCAGAGGTGGAGAGCCCTTTTCAGGGCGCTGCAGTGGATGCGCAGCAGACCTG 300
DB 603 CACCAGGAAGTGGAGAGCCCTTTCCAAAGGCGCTTGCAGTGGAAATGGGAGCAAGACCTG 662
QY 301 CAGGACGTGTCCATCACTGTGCTCAAGCTCACTCTGAACGACTCTGCGCTCTACACCTGC 360
DB 663 CAGGACGTATCCATCACTGTACTCAATGTCACTTTGAATGACTCTGCGCTCTACACATGC 722
QY 361 AATGTGTCGCGGAGTTTGAAGTGGAGCGCATCGGCCCTTTTGTGAAGAGACGCGGCTG 420
DB 723 AATGTGTCCAGGAGTTTGAATTCAGGCGCACACAGGCGCTTTTGTGAAGACGCGGACTG 782
QY 421 ATCCCCCTAAGAGTCAAGGAGGCTGGAGAGCTTCACTCTGTGTCTCAGAAATC 480
DB 783 ATACCTTTGGAGTCACTGAAGAGGCGGGAAGACTTCACTCCCGTGGTCTCGAAATC 842
QY 481 ATGATGTACATCTCTCTGCTTCTCCTCAACCTGTGGCTGCTCATCGAGATGATATATGC 540
DB 843 ATGATGTACATCTCTCTGCTTCTCCTCACTGTGTGGCTGTTTATGAGATGATCTATGC 902
QY 541 TACAGAAAGGTCTCAAAAGCCGAAGAGCGAGCCCAAGAAACCGCTCTGACTACCTTGGC 600
DB 903 TACAGAAAGGTCTCTAAGGCCGAAGAGCGAGCACAGGAAATGCGTCTGACTACCTTGGT 962
QY 601 ATCCCATCTGAGAACAGGAGAACTCTGCGGTACCATGAGGGAATA 647
DB 963 ATCCCTTCAGAGAACAGGAGAACTCTGTGTACCTCTGTGGGGAATA 1009

RESULT 4

US-10-029-191-22
; Sequence 22, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A. J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2632
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-22

Query Match 82.8%; Score 536.6; DB 5; Length 2632;
Best Local Similarity 89.3%; Pred. No. 4.5e-164;
Matches 578; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 1 ATGCTGCTCCCTTCAATAGATTCTTCCCTGCTGCTTCTCTGCTGCTTATCTACTGGTTCAGT 60
DB 78 ATGCTGCTCCCTTCAACAGATTCTTCCCTAGCTTCTCTAGTGTCTATCTACTGGTTCAGA 137
QY 61 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGAGCGGAGCGCTGCAGGGCAACCCC 120
DB 138 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGAGCGGAGCGGTGCAGGGCAATCCC 197
QY 121 ATGAAGTGCCTGCTATCTCTGATGAAGAGAGAGGTGGAGGCCACACCGTGGTG 180
DB 198 ATGAAGTGCAGTGTGATCTCTGATGAAGAGAGAGGTGGAGGCCACACCTGTGGTG 257
QY 181 GAATGGTTCACAGCCCGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 240
DB 258 GAGTGGTTCACAGCCCTGAGGGCGGTAAAGATTTCCTTATATATGATATCGGAATGGC 317
QY 241 CACCAGGAGTGGAGAGCCCTTTTCAGGGCGCTGCAGTGGAAATGGCAGGACCTG 300

DB 318 CACCAGGAAGTGGAGAGCCCTTTCCAAAGGCGCTTGCAGTGGAAATGGGAGCAAGACCTG 377
QY 301 CAGGACGTGTCCATCACTGTGCTCAAGCTCACTCTGAACGACTCTGCGCTCTACACCTGC 360
DB 378 CAGGACGTATCCATCACTGTACTCAATGTCACTTTGAATGACTCTGCGCTCTACACATGC 437
QY 361 AATGTGTCGCGGAGTTTGAAGTGGAGCGCATCGGCCCTTTTGTGAAGAGACGCGGCTG 420
DB 438 AATGTGTCCAGGAGTTTGAATTCGAGGCGCACACAGGCGCTTTTGTGAAGACGCGGACTG 497
QY 421 ATCCCCCTAAGAGTCAAGGAGGCTGGAGAGACTTCACTCTGTGTCTCAGAAATC 480
DB 498 ATACCTTTGGAGTCACTGAAGAGGCGGGAAGACTTCACTCCCGTGGTCTCGAAATC 557
QY 481 ATGATGTACATCTCTCTGCTTCTCCTCAACCTGTGGCTGCTCATCGAGATGATATATGC 540
DB 558 ATGATGTACATCTCTCTGCTTCTCCTCACTCTGTGGCTGTTTATGAGATGATCTATGC 617
QY 541 TACAGAAAGGTCTCAAAAGCCGAAGAGCGAGCCCAAGAAACCGCTCTGACTACCTTGGC 600
DB 618 TACAGAAAGGTCTCTAAGGCCGAAGAGCGAGCACAGGAAATGCGTCTGACTACCTTGGT 677
QY 601 ATCCCATCTGAGAACAGGAGAACTCTGCGGTACCATGAGGGAATA 647
DB 678 ATCCCTTCAGAGAACAGGAGAACTCTGTGTACCTCTGTGGGGAATA 724

RESULT 5

US-10-029-191-1
; Sequence 1, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A. J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3108
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-1

Query Match 82.8%; Score 536.6; DB 5; Length 3108;
Best Local Similarity 89.3%; Pred. No. 4.8e-164;
Matches 578; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 1 ATGCTGCTCCCTTCAATAGATTCTTCCCTGCTGCTTCTCTGCTGCTTATCTACTGGTTCAGT 60
DB 78 ATGCTGCTCCCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGTCTATCTACTGGTTCAGA 137
QY 61 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGAGCGGAGCGCTGCAGGGCAACCCC 120
DB 138 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGAGCGGAGCGGTGCAGGGCAATCCC 197
QY 121 ATGAAGTGCCTGCTATCTCTGATGAAGAGAGAGGTGGAGGCCACACCGTGGTG 180
DB 198 ATGAAGTGCAGTGTGATCTCTGATGAAGAGAGAGGTGGAGGCCACACCTGTGGTG 257
QY 181 GAATGGTTCACAGCCCGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 240
DB 258 GAGTGGTTCACAGCCCTGAGGGCGGTAAAGATTTCCTTATATATGATATCGGAATGGC 317
QY 241 CACCAGGAGTGGAGAGCCCTTTTCAGGGCGCTGCAGTGGAAATGGCAGGACCTG 300

Db 318 CACCAGGAAGTGGAGAGCCCTTCAAGGCCGTCTGCAGTGAATGGAGCAAGACCTG 377
Qy 301 CAGACGTGTCCATCACTGTGCTCAACGTCTACTCTGAACGACTCTGCGCTCTACACCTGC 360
Db 378 CAGACGCTATCCATCACTCACTCAATGTCTACTTTGAATGACTCTGCGCTCTACACATGC 437
Qy 361 AATGTGTCGGGAGTTTGTAGTTTGTAGCGCATCGGCCCTTTGTGAAGACGACGCGCTG 420
Db 438 AATGTGTCAGGAGTTTGAATTCGAGGACACAGGCTTTTGTGAAGACACAGACTG 497
Qy 421 ATCCCCCTTAAGACTCACCGAGAGGCTGGAGAGACTTCACCTCTGTGGTCTCAGAAATC 480
Db 498 ATACCTTTGCGAGTCACTGAAGAGCGGAGAGACTTCACCTCGTGGTCTCGGAAATC 557
Qy 481 ATGATGTACATCTCTCTGCTTCTTCTCCTCACCCTGTGGCTGCTCATCGAGATGATATTC 540
Db 558 ATGATGTACATCTCTCTGCTTCTTCTCCTCACCTTGTGGCTGTTTATGTAGATGATATTC 617
Qy 541 TACAGAAAGGTCTCAAAAGCCGAGAGCGACGCCCAAGAAACGGCTCTGACTACCTTTGCC 600
Db 618 TACAGAAAGGTCTCTAAGGCCGAGAGGACGACAGGAAATGCGTCTGACTACCTTGCT 677
Qy 601 ATCCCATCTGAGAACAAAGGAGAACTCTCGGTACCGTACGAGTGGAGGAATA 647
Db 678 ATCCCTTCAGAGAACAAAGGAGAACTCTGTGTACCTCTGTGGAGGAATA 724

RESULT 6

US-10-450-763-22568
; Sequence 22568, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22568
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (518)..(1051)
; OTHER INFORMATION: 91% homologous to Homo sapiens voltage-gated sodium channel
; OTHER INFORMATION: beta-3 subunit, accession number AJ243396, Smith-Waterman Score=826
US-10-450-763-22568

Query Match 82.5%; Score 534.8; DB 9; Length 1195;
Best Local Similarity 95.7%; Pred. No. 1.3e-163;
Matches 572; Conservative 0; Mismatches 22; Indels 4; Gaps 2;
Qy 1 ATGCTGCTTCCATAGATTGTTTCCCTCGCTTCTCTCGTCTTATCTACTGGGTCAGT 60
Db 463 ATGCTGCTTCCATAGATTGTTTCCCTCGCTTCTCTCGTCTTATCTACTGAGTCAGT 522
Qy 61 GTCTGCTTCCCTGTGTGTGTGAA--GTGCTCTCGAGACGAGCGCTGCA--GGGCAA 116
Db 523 GTCTGCTTCCCTGTGTGTGGGGAAGTCCCTTAGAAAACGGGGCGGCGCACGGCTAA 582
Qy 117 CCCATGAAGCTGCGCTGATCTCTGCAATGAAGAGAGAGGAGTGTGAGGCCACACCGGT 176
Db 583 CCCATGAAGCTGCGCTGATCTCTGCAATGAAGAGAGAGGAGTGTGAGGCCACACCGGT 642
Qy 177 GGTGGAATGTTCTACAGCCCGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAA 236

Db 643 GGTGGAATGTTCTACAGGCCCGAGGCGGTAAAGATTTCCTTATTTACGAGTATCGAA 702
Qy 237 TGGCCACAGGAGGTGGAGAGCCCTTTTCAAGGGCGCTCGAGTGAATGGCAGCAAGGA 296
Db 703 TGGCCACAGGAGGTGGAGAGCCCTTTTCAAGGGCGCTCGAGTGAATGGCAGCAAGGA 762
Qy 297 CTGTGAGGAGGTGCCATCACTGTGCTCAACGTCACCTCTCAACGACTCTGGCCCTCTACAC 356
Db 763 CTGTGAGGAGGTGCCATCACTGTGCTCAACGTCACCTCTCAACGACTCTGGCCCTCTACAC 822
Qy 357 CTGCAATGTGTCCCGGAGTTTGTAGTTTGTAGGCGCATCGGCCCTTTGTGAAGACGACGCG 416
Db 823 CTGCAATGTGTCCCGGAGTTTGTAGTTTGTAGGCGCATCGGCCCTTTGTGAAGACGACGCG 882
Qy 417 GCTGATCCCCCTTAAGAGTCAACGAGGAGGTGGAGAGGACTTCACCTCTGTGTCTCAGA 476
Db 883 GCTGATCCCCCTTAAGAGTCAACGAGGAGGTGGAGAGGACTTCACCTCTGTGTCTCAGA 942
Qy 477 AATCATGATGTACATCTCTGTGTCTTCTCCCTCACCTCTGCTGCTCATCGAGATGATATA 536
Db 943 AATCATGATGTACATCTCTGTGTCTTCTCCCTCACCTCTGCTGCTCATCGAGATGATATA 1002
Qy 537 TTGCTACAGAAAGGTCTCAAAAGCCGAGAGGCGAGCCCAAGAAAACCGCTCTGACTAC 594
Db 1003 TTGCTACAGACAGGTCTCAAAAGCCGAGAGGCGAGCCCAAGAAAACCGCGCAGGAAC 1060

RESULT 7

US-10-029-191-21
; Sequence 21, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-21

Query Match 82.5%; Score 534.6; DB 5; Length 645;
Best Local Similarity 89.3%; Pred. No. 1.2e-163;
Matches 576; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
Qy 1 ATGCTGCTTCCATAGATTGTTTCCCTCGCTTCTCTCGTCTTATCTACTGGGTCAGT 60
Db 1 ATGCTGCTTCCATAGATTGTTTCCCTCGCTTCTCTAGTGTCTATCTACTGGGTCAGA 60
Qy 61 GTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGACGAGGCGGTGAGGGCAACCCC 120
Db 61 GTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGACAGAGCGGTGAGGGCAATCCC 120
Qy 121 ATGAAGTGGCGTGCATCTCTGCAATGAAGAGAGAGGAGTGTGAGGCCACACCGTGTG 180
Db 121 ATGAAGTGGAGTGCATCTCTGCAATGAAGAGGAGGAGTGTGAGGCCACACCTGTGTG 180
Qy 181 GAATGTTCTACAGCCCGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGCG 240
Db 181 GAGTGGTCTACAGCCCTGAGGCGGTAAAGATTTCCTTATATGATATCGGAATGCG 240
Qy 241 CACGAGGAGTGTGAGAGCCCTTTTCAAGGGCGCTTCAAGTGTGAATGGCAGCAAGGACCTG 300

	Query Match	60.6%;	Score 392.6;	DB 9;	Length 3531;
	Best Local Similarity	99.0%;	Pred. No. 5.4e-117;		
	Matches 395;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	47	TCTACTGGGTCAGTCTGCTTCCTCTGTGTGTGGAGTGCCTTCGAGACGGAGGCCG	106		
Db	2951	TCAGGTGTGCAGTGTCTGCTTCCTCTGTGTGTGGAAAGTGCCCTTCGAGACGGAGGCCG	3010		
Qy	107	TGCAGGCGCAACCCCATGAAGCTGGCGCTGCATCTCTCTGCATCAAGAGAGAGAGGTGGAGG	166		
Db	3011	TGCAGGCGCAACCCCATGAAGCTGGCGCTGCATCTCTCTGCATCAAGAGAGAGAGGTGGAGG	3070		
Qy	167	CCACCACGGTGGTGGAAATGGTTTACAGGCCCGAGGGCGGTAAAGATTTCTTTATTTACG	226		
Db	3071	CCACACGGTGGTGGAAATGGTTTACAGGCCCGAGGGCGGTAAAGATTTCTTTATTTACG	3130		

Query Match	55.9%;	Score 362;	DB 10;	Length 600;
Best Local Similarity	100.0%;	Pred. No. 2.8e-107;		
Matches 362;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	287	GCAGCAGGACCTGCAGGAGCTGCCATCAGCTGTGCTCAACGTCACCTCTGAAACGACTCTG	346	
Db	1	GCAGCAGGACCTGCAGGAGCTGCCATCAGCTGTGCTCAACGTCACCTCTGAAACGACTCTG	60	
Qy	347	GCCTCTACACCTGCAATGTGCCGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGA	406	
Db	61	GCCTCTACACCTGCAATGTGCCGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGA	120	
Qy	407	AGACGACGGCGGTGATCCCCCTAAGAGTCACCGAGGAGCTCGAGAGGACTTCACCTCTG	466	
Db	121	AGACGACGGCGGTGATCCCCCTAAGAGTCACCGAGGAGCTCGAGAGGACTTCACCTCTG	180	
Qy	467	TGCTCTCAGAAATCATGATGTACATCCTTCTGGTCTTCTCACCCTGTGGCTGCATCG	526	
Db	181	TGCTCTCAGAAATCATGATGTACATCCTTCTGGTCTTCTCACCCTGTGGCTGCATCG	240	
Qy	527	AGATGATATATTGCTACAGAAAGGTCTCAAAACCGAGAGCGAGCGCCCAAGAAAACGGCT	586	
Db	241	AGATGATATATTGCTACAGAAAGGTCTCAAAACCGAGAGCGAGCGCCCAAGAAAACGGCT	300	
Qy	587	CTCAGCTACCTTGGCATCCCATCTGAGAACCAAGGAGAACTCTCGGTCACCAAGTGGAGGAAT	646	
Db	301	CTCAGCTACCTTGGCATCCCATCTGAGAACCAAGGAGAACTCTCGGTCACCAAGTGGAGGAAT	360	
Qy	647	AG 648		
Db	361	AG 362		

RESULT 10
US-11-060-756-2817
: Sequence 2817, Application US/11060756

Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2817
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2817

Query Match 55.9%; Score 362; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 2.8e-107;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	287	GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTG	346
Db	1	GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTG	60
Qy	347	GCCTCTACACCTGCAATGTGTCGCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGA	406
Db	61	GCCTCTACACCTGCAATGTGTCGCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGA	120
Qy	407	AGACGACGCGGCTGATCCCTTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACTCTG	466
Db	121	AGACGACGCGGCTGATCCCTTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACTCTG	180
Qy	467	TGGTCTCAGAAATCATGATGTACATCCTTCTGCTTCTTCCATCCCTTGGCTGCTCATCG	526
Db	181	TGGTCTCAGAAATCATGATGTACATCCTTCTGCTTCTTCCATCCCTTGGCTGCTCATCG	240
Qy	527	AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCAGCAAGAAACCGGT	586
Db	241	AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCAGCAAGAAACCGGT	300
Qy	587	CTGACTACCTTGCATCCCATCTGAGAAACAGGAGAACTCTGCGGTACCACTGGAGGAAT	646
Db	301	CTGACTACCTTGCATCCCATCTGAGAAACAGGAGAACTCTGCGGTACCACTGGAGGAAT	360
Qy	647	AG 648	
Db	361	AG 362	

RESULT 11
US-11-060-756-7088
; Sequence 7088, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7088
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7088

Query Match 55.9%; Score 362; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 2.8e-107;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	287	GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTG	346
Db	1	GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTG	60
Qy	347	GCCTCTACACCTGCAATGTGTCGCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGA	406
Db	61	GCCTCTACACCTGCAATGTGTCGCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGA	120
Qy	407	AGACGACGCGGCTGATCCCTTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACTCTG	466
Db	121	AGACGACGCGGCTGATCCCTTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACTCTG	180
Qy	467	TGGTCTCAGAAATCATGATGTACATCCTTCTGCTTCTTCCATCCCTTGGCTGCTCATCG	526
Db	181	TGGTCTCAGAAATCATGATGTACATCCTTCTGCTTCTTCCATCCCTTGGCTGCTCATCG	240
Qy	527	AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCAGCAAGAAACCGGT	586
Db	241	AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCAGCAAGAAACCGGT	300
Qy	587	CTGACTACCTTGCATCCCATCTGAGAAACAGGAGAACTCTGCGGTACCACTGGAGGAAT	646
Db	301	CTGACTACCTTGCATCCCATCTGAGAAACAGGAGAACTCTGCGGTACCACTGGAGGAAT	360
Qy	647	AG 648	
Db	361	AG 362	

RESULT 12
US-11-060-756-7089
; Sequence 7089, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7089
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7089

Query Match 55.9%; Score 362; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 2.8e-107;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	287	GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTG	346
Db	1	GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTG	60
Qy	347	GCCTCTACACCTGCAATGTGTCGCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGA	406
Db	61	GCCTCTACACCTGCAATGTGTCGCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGA	120
Qy	407	AGACGACGCGGCTGATCCCTTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACTCTG	466
Db	121	AGACGACGCGGCTGATCCCTTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACTCTG	180
Qy	467	TGGTCTCAGAAATCATGATGTACATCCTTCTGCTTCTTCCATCCCTTGGCTGCTCATCG	526
Db	181	TGGTCTCAGAAATCATGATGTACATCCTTCTGCTTCTTCCATCCCTTGGCTGCTCATCG	240
Qy	527	AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCAGCAAGAAACCGGT	586
Db	241	AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCAGCAAGAAACCGGT	300

Qy 587 CTGACTACCTTGGCATCCCATCTGAGAACCAAGGAGAACTCTGCGGTACCAAGTGGAGAAAT 646
Db 301 CTGACTACCTTGGCATCCCATCTGAGAACCAAGGAGAACTCTGCGGTACCAAGTGGAGAAAT 360
Qy 647 AG 648
Db 361 AG 362

RESULT 13

US-09-925-065A-774904
; Sequence 774904, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 774904
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapiens

Query Match 35.4%; Score 229.2; DB 4; Length 545;
Best Local Similarity 95.9%; Pred. No. 6.4e-64;
Matches 234; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 212 ATTTCTCTATTACGAGTATCGGAATGCCACAGGAGGTGGAGAGCCCTTTTCAGGGGC 271
Db 136 ATCTGCAGATTACGAGTATCGGAATGCCACAGGAGGTGGAGAGCCCTTTTCAGGGGC 195
Qy 272 GCCTGCAGTGAATGGCAGCAAGACCTGCGAGGACGTGTCCATCACTGTGCTCAACGTCA 331
Db 196 GCCTGCAGTGAATGGCAGCAAGACCTGCGAGGACGTGTCCATCACTGTGCTCAACGTCA 255
Qy 332 CTCTGAACGACTCTGGCTCTACACCTGCAATGTCTCCGGAGTTTGGTTGAGGGCC 391
Db 256 CTCTGAACGACTCTGGCTCTACACCTGCAATGTCTCCGGAGTTTGGTTGAGGGCC 315
Qy 392 ATCGGCCCTTTTGAAGACGACGCGGTGTATCCCTTAAGAGTCAACGAGGAGCTGGAG 451
Db 316 ATCGGCCCTTTTGAAGACGACGCGGTGTATCCCTTAAGAGTCAACGAGGAGGTGAGG 375
Qy 452 AGGA 455
Db 376 CTGA 379

RESULT 14

US-10-450-763-22566
; Sequence 22566, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763

; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22566
; LENGTH: 621
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (40)..(282)
; OTHER INFORMATION: 95% homologous to Rattus norvegicus voltage-gated sodium
; OTHER INFORMATION: channel beta-3 subunit, accession number AJ243395, Smith-Waterman
; OTHER INFORMATION: Score=397.
US-10-450-763-22566

Query Match 34.6%; Score 224.4; DB 9; Length 621;
Best Local Similarity 99.6%; Pred. No. 2.5e-62;
Matches 225; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 220 ATTTACGAGTATCGGAATGCCACAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTGCAG 279
Db 58 ATTTACGAGTATCGGAATGCCACAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTGCAG 117
Qy 280 TGGATGGCAGCAAGGACCTGCGAGGAGTCCATCACTGCTCAACGTCACCTCTGAAC 339
Db 118 TGGATGGCAGCAAGGACCTGCGAGGAGTCCATCACTGCTCAACGTCACCTCTGAAC 177
Qy 340 GACTCTGGCTCTACACCTGCAATGTCTCCGGAGTTTGAGTTGAGGGCGCATCGGCC 399
Db 178 GACTCTGGCTCTACACCTGCAATGTCTCCGGAGTTTGAGTTGAGGGCGCATCGGCC 237
Qy 400 TTTGTGAAGACGACGCGGTGTATCCCTTAAGAGTCAACGAGGAGG 445
Db 238 TTTGTGAAGACGACGCGGTGTATCCCTTAAGAGTCAACGAGGAGG 283

RESULT 15

US-10-029-191-23
; Sequence 23, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Lepus Sp.
US-10-029-191-23

Query Match 22.9%; Score 148.2; DB 5; Length 657;
Best Local Similarity 57.7%; Pred. No. 2e-37;
Matches 333; Conservative 0; Mismatches 223; Indels 21; Gaps 3;
Qy 76 TGTGTGAAGTCCCTCGGAGACGAGGCGGTGGAGGCAACCCCATCAACGCTGCCTGC 135
Db 61 TGCCTGAGGTGGACTCGGAGACCGGCGGTGACCGGATGACCTTCAAAATTTCTGTGC 120

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Qy 136 ATCTCTGATGTAAGAGAGAGAGGTGGAGGCCACACGGTGGTGGAAATGGTTCTACAGG 195
    |||||
Db 121 ATCTCTGCAAGCGCCGAGGAGACACACGCCGAGACCTTTCAGGAGTGACCTTCGCG 180
    |||||
Qy 196 CCCGAGGCGGTAAAGATT-----TCCTTATTTACGAGTATCGGAATGGCCACCAG 246
    |||||
Db 181 CAGAAGGGCACTGAGGAGTTCTGTCAGATCTCGCTATGAGAACGAGGTGCTGCAGCTG 240
    |||||
Qy 247 GAGTGGAGAGCCCTTTCAGGGGGCGCTGCAGTGGAAATGGCAG-----CAAGGAC 297
    |||||
Db 241 GAGGAAGACGAGCGCTTTGAGGGCGCGTGTGGAACGGCAGCCGGGGCACCAGGAC 300
    |||||
Qy 298 CTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTGGCCTCTACACC 357
    |||||
Db 301 CTGCAGGACCTGTCCATCTTCAATCACCATGTCACTTACAACCACTCGGGGACTACGAG 360
    |||||
Qy 358 TGCAATGTGTCGCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGCGG 417
    |||||
Db 361 TGCCATGTCTACCGCCTGCTCTCCTTCGAAACTACGAGCACAAACCCAGCGTGTCAAG 420
    |||||
Qy 418 CTGATCCCCCTAAGAGTCAACGAGAGGCTGGAGAGGACTTCACCTCTGTGGTCTCAGAA 477
    |||||
Db 421 AAGATCCACCTGGAGGTGGTGGACAAGGCCAACACAGAGACATGGCATCCATCGTGTGCGAG 480
    |||||
Qy 478 ATCATGATGTACATCCTTCTGCTCTTCTCCTCACCTGTGGCTGCTCATCGAGATGATATAT 537
    |||||
Db 481 ATCATGATGTACGTCTCATCGTGTGTGACCATCTGGCTCGTGGCGGAGATGGTGTAC 540
    |||||
Qy 538 TGCTACAGAAAGGTCTCAAAAGCCGGAAGAGGCA---GCCCAAGAAACCGCTCTGACTAC 594
    |||||
Db 541 TGCTACAAGAAGATCGCGGCCCCACGAGGAGCGCGGCGCAGAGAGAACGCCCTCGGAATAC 600
    |||||
Qy 595 CTGGCCATCCCATCTGAGAACAAAGGAACTCTGCGG 631
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Db 601 TTGGCCATCACCTCAGAAAGCAAGAAATTGCAAGG 637
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

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Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	648	100.0	1261	6 US-10-374-954-8	Sequence 8, Appli
2	143.8	22.2	1335	6 US-10-374-954-4	Sequence 4, Appli
3	130.4	20.1	880	6 US-10-750-185-44336	Sequence 4336, A
4	57.8	8.9	1497	6 US-10-750-185-44339	Sequence 44339, A
5	51	7.9	150468	7 US-11-112-908-56	Sequence 56, Appl
6	51	7.9	193789	7 US-11-112-908-55	Sequence 55, Appl
7	38	5.9	1689	6 US-10-507-928-9	Sequence 9, Appli
8	38	5.9	1689	6 US-10-507-928-11	Sequence 11, Appl
9	38	5.9	1689	7 US-11-029-465-9	Sequence 9, Appli
10	38	5.9	1689	7 US-11-029-465-11	Sequence 11, Appl
11	36.2	5.6	673	7 US-11-080-991-111	Sequence 111, App
12	36.2	5.6	1371	6 US-10-131-826A-487	Sequence 487, App
13	35.4	5.5	2849	6 US-10-131-826A-371	Sequence 371, App
14	34	5.2	175100	7 US-11-121-086-21	Sequence 21, Appl
15	33.8	5.2	1485	6 US-10-750-185-61749	Sequence 61749, A
c 16	32.8	5.1	1506	6 US-10-750-185-30397	Sequence 30397, A
c 17	32.8	5.1	2236	6 US-10-131-826A-381	Sequence 381, App
18	32.4	5.0	33737	6 US-10-276-233A-7	Sequence 7, Appli
c 19	32.4	5.0	162085	7 US-11-121-086-7	Sequence 7, Appli
20	32.2	5.0	4104	6 US-10-131-826A-449	Sequence 449, App
21	32	4.9	762	6 US-10-821-234-586	Sequence 586, App
c 22	32	4.9	2257	6 US-10-750-185-46007	Sequence 46007, A
23	31.8	4.9	2454	6 US-10-750-185-30593	Sequence 30593, A

ALIGNMENTS

RESULT 1

US-10-374-954-8
; Sequence 8, Application US/10374954
; Publication No. US20050260576A1

; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University

; APPLICANT: George, Alfred L.
; APPLICANT: Lossin, Christoph

; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; FILE REFERENCE: 1242/41/2

; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25

; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25

; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2

; SEQ ID NO 8
; LENGTH: 1261

; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: CDS

; LOCATION: (376)..(1023)
US-10-374-954-8

Query Match 100.0%; Score 648; DB 6; Length 1261;
Best Local Similarity 100.0%; Pred. No. 9.5e-181;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGCCTGCCTTCAATAGATTGTTTCCCTCGCTTCTCTCGTCTTCTACTGGTCACT	60
Db	376	ATGCCTGCCTTCAATAGATTGTTTCCCTCGCTTCTCTCGTCTTCTACTGGTCACT	435
Qy	61	GTCTGCTTCCCTGTGTGTGGAAAGTCCCTCGGAGACGGAGCCGTCGAGGGCAACCCC	120
Db	436	GTCTGCTTCCCTGTGTGTGGAAAGTCCCTCGGAGACGGAGCCGTCGAGGGCAACCCC	495
Qy	121	ATGAAGTCGGCTGCATCTCTCGATGAGAGAGAGAGTGGAGGCCACACGGTGTG	180
Db	496	ATGAAGTCGGCTGCATCTCTCGATGAGAGAGAGTGGAGGCCACACGGTGTG	555
Qy	181	GAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC	240
Db	556	GAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC	615

241	Qy	CAC	CAG	AGG	TGG	AGAG	CCCC	CTTT	CAG	GGG	CGC	CTG	CAG	TGG	AAT	TGG	CAG	AAG	AC	CTG	300
616	Db	CAC	CAG	AGG	TGG	AGAG	CCCC	CTTT	CAG	GGG	CGC	CTG	CAG	TGG	AAT	TGG	CAG	AAG	AC	CTG	675
301	Qy	CAG	ACG	TG	CT	CA	CT	GT	CG	TCA	CT	CT	G	AC	GA	CT	CT	G	GG	CCT	360
676	Db	CAG	ACG	TG	CT	CA	CT	GT	CG	TCA	CT	CT	G	AC	GA	CT	CT	G	GG	CCT	735
361	Qy	AAT	GTG	TCC	CGG	GAG	TTT	GAG	T	TG	AGG	CG	CAT	CGG	CC	CTT	TG	AAG	AC	GAC	420
736	Db	AAT	GTG	TCC	CGG	GAG	TTT	GAG	T	TG	AGG	CG	CAT	CGG	CC	CTT	TG	AAG	AC	GAC	795
421	Qy	AT	CCCC	CT	A	G	A	G	T	C	A	C	G	A	G	A	G	G	C	T	480
796	Db	AT	CCCC	CT	A	G	A	G	T	C	A	C	G	A	G	A	G	G	C	T	855
481	Qy	AT	G	A	T	G	A	T	A	C	T	T	C	T	C	A	C	C	T	G	540
856	Db	AT	G	A	T	G	A	T	A	C	T	T	C	T	C	A	C	C	T	G	915
541	Qy	TAC	A	G	A	A	G	G	T	CT	CA	A	A	G	CG	A	G	A	G	CG	600
916	Db	TAC	A	G	A	A	G	G	T	CT	CA	A	A	G	CG	A	G	A	G	CG	975
601	Qy	AT	CCC	AT	CT	G	A	A	C	A	G	A	A	CT	CT	CG	G	T	A	C	648
976	Db	AT	CCC	AT	CT	G	A	A	C	A	G	A	A	CT	CT	CG	G	T	A	C	1023

```

RESULT 2
US-10-374-954-4
; Sequence 4, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L.
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25) .. (681)
US-10-374-954-4

```

Query Match	22.2%	Score 143.8	DB 6	Length 1335
Best Local Similarity	56.9%	Prod. No. 1e-32		
Matches 334	Conservative 0	Mismatches 232	Indels 21	Gaps 3
Qy	66	CTTCCCTGTGTGTGGAAATGCCCTCGAGACGAGGCGCTGAGGGCAACCCCATGAA	125	
Db	75	CTCGGGGGCTGCGCTGGAGGTGGACTCGAGACCGAGGCCGTGTATGGGATGACCTTCAA	134	
Qy	126	GCTCGGCTGCATCTCCTGCATGAAGAGAGAGGTGGAGGCCACCGGTGGTGGAAATG	185	
Db	135	AATTCTTTTGCATCTCTGTCAAGCGCCGACGACCAACGCTGAGACCTTCACCGAGTG	194	
Qy	186	GTTCTTACAGGCGCAGGGCGGTAAAGATT-----TCCTTATTTACGATATCGGAA	236	
Db	195	GACCTTCGCCAGAAAGGCACTGAGGAGTGTGTCAAGATCTCGCGCTATGAGAATGAGGT	254	
Qy	237	TGGCCACGAGAGGTGGAGAGCCCTTTTCAGGGGCGCTTCAGGTGGAAATGGCAG-----	290	

255	Db	GTTCGACCTGGAGGAGATGAGCGCTTCGAGGGCGCGTGTGTGGAAATGGCAGCCGGGG	314
291	Qy	---CAAGGACCTGCAGGACGTGTCCATCAGCTGTGTCAACGTCACTCTTGAACGACTCTGG	347
315	Db	CACCAAGAAGCTGCAGGATCTGTCTAICTTTCATCACCAGTGCACCTACCAACCTTCGG	374
348	Qy	CTTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGGGCATCGGCCCTTTGTGAA	407
375	Db	CGACTACGAGTGCCACGCTCTACCGCTGCTCTTCTTCGAAAACTACGAGCAACAACCCAG	434
408	Qy	GACGACCGGCTGATCCCTTAAAGATCACCGAGGAGCTGGAGAGGACTTACCTCTGT	467
435	Db	CGTCGTCAAGAAGATCACACTTGAGGTAGTGGACAAGGCCAACAGAGACATGGCATCCAT	494
468	Qy	GGTCTCAGAAGATCATGATGTATCATCTTCTGTGTTCTCTCACCTGTGGCTGCTCATCGA	527
495	Db	CGTGTCTGAGATCATGATGATGATGTGCTCATTTGTGTTGACCATATGGCTCGTGGCAGA	554
528	Qy	GATGATATATTGTCTACAGAAGGTCTCAAAAAGCCGAAGAG---GCAGCCCCAAGAAAACGC	584
555	Db	GATGATTTACTGCTACAAGAAGATCGCTGCGCCACCGAGACTGTGCACAGGAGAAATGC	614
585	Qy	GTCTGACTACTTGGCCATCCCATCTGAGAAACAAGAGAACTCTGGCG	631
615	Db	CTCGGAATACCTGGCCATCACTCTGAAGCAAAAGAGAACTGCACGG	661

```

RESULT 3
US-10-750-185-44336
; Sequence 44336, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44336
; LENGTH: 880
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-44336

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Query Match	20.1%;	Score 130.4;	DB 6;	Length 880;
Best Local Similarity	82.8%;	Pred. No. 7.3e-29;		
Matches 149;	Conservative 0;	Mismatches 31;	Indels 0;	Gaps 0
Qy	414	GC	GCTGATCCCC	TAAAGATCACCGAGGAGGCTGGAGAGCACTTCACTCTGTGGTCTC 473
Db	412	GC	GCAATCTC	GAGTCTCATCTCTCCCTTGACCTGGAGAGCACTTCACTCTGTGGTCTC 471
Qy	474	AGA	AATCATGATG	TACATCTCTTCTGGTCTTCTCTCACCTGTGGCTGTCTATCGAGATGAT 533
Db	472	AGA	AATCATGATG	TACATCTCTCTGGTCTTCTCTCACTCTGTGGCTGTCTATTTAGATGAT 531
Qy	534	ATA	TGTCTACAGAAAG	GTCTCAAAAGCGGAGAGCGACGCCCAAGAAACGGCGTCTGTGACTA 593
Db	532	ATA	TGTCTACAGAAAG	GTCTCGAAGGCTGAAGAGCGCGCCCAAGAAATGCGTAAGTCCA 591

RESULT 4

US-10-750-185-44339

Sequence 44339, Application US/10750185

Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44339
; LENGTH: 1497
; TYPE: DNA
; ORGANISM: Bovine 19866880940727
US-10-750-185-44339

Query Match 8.9%; Score 57.8; DB 6; Length 1497;
Best Local Similarity 89.9%; Pred. No. 1.8e-07;
Matches 62; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 580 AACCGCTGCTGACTACCTTCCATCCCATCTGAGAACAGGAGAACTCTGCGGTACCAAGTG 639
Db |||||
Qy 1289 AACAGGTCTGACTACTGCGCATCCCATCGGATCGGAGAACAAAGAGAACTCTGCACTCCCAAGTG 1348
Db |||||

Qy 640 GAGGAATAG 648
Db |||||
Qy 1349 GAGGAATAG 1357
Db |||||

RESULT 5
US-11-112-908-56
; Sequence 56, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56
; LENGTH: 150468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-56

Query Match 7.9%; Score 51; DB 7; Length 150468;
Best Local Similarity 58.1%; Pred. No. 0.00011;
Matches 90; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 66 CTTCCCTGTGTGTGGAAGTGCCTCGGAGACGGAGCGCGTGCAGGCGCAACCCCATGAA 125
Db |||||
Qy 52602 CTGCGGGGGCTGCGTGGAGGTGGACTCGGAGACCGAGCGCGTGTATGGATGACCTTCAA 52661
Db |||||
Qy 126 GCTCGCTGTCATCTCTCGCATGAAGAGAGAGAGAGGTGGAGCCACCGTGGTGGATG 185
Db |||||

Db 52662 AATCTTTGTCATCTCTGCAAGCGCGCAGAGACAACGCTGAGACCTTACCGAGTG 52721
Qy 186 GTTCTACAGCGCCGAGCGGGGTAAGATTTCCTTA 220
Db |||||
Db 52722 GACCTTCCCGCAGAGAGGCACTGAGGAGTTTGTC 52756
Db |||||

RESULT 6

US-11-112-908-55
; Sequence 55, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55
; LENGTH: 193789
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-55

Query Match 7.9%; Score 51; DB 7; Length 193789;
Best Local Similarity 58.1%; Pred. No. 0.00012;
Matches 90; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 66 CTTCCCTGTGTGTGGAAGTGCCTCGGAGACGGAGCGCGTGCAGGCGCAACCCCATGAA 125
Db |||||
Qy 126 GCTCGCTGTCATCTCTCGCATGAAGAGAGAGAGAGGTGGAGCCACCGTGGTGGATG 185
Db |||||
Qy 186 GTTCTACAGCGCCGAGCGGGTAAAGATTTCCTTA 220
Db |||||
Qy 102907 GACCTTCCCGCAGAGAGGCACTGAGGAGTTTGTC 102941
Db |||||

RESULT 7

US-10-507-928-9
; Sequence 9, Application US/10507928
; Publication No. US20050266024A1
; GENERAL INFORMATION:
; APPLICANT: POWDERMED LIMITED AND GLAXO GROUP LIMITED
; TITLE OF INVENTION: ADJUVANT
; FILE REFERENCE: N.88232B GCW
; CURRENT APPLICATION NUMBER: US/10/507,928
; CURRENT FILING DATE: 2004-09-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence of RT insert of p7077-RT3
US-10-507-928-9

Query Match 5.9%; Score 38; DB 6; Length 1689;
Best Local Similarity 62.8%; Pred. No. 0.13;

Qy	258	CCCTTTTCAGGGGCGCTGCAGTGGAAATGGCAGCAAGGACCTGCAGGACCTGTCGATCAC	317
Db	295	GCGGTTTAAGGACCGGGTGTCTTGGATGGGAATCCTGACGGGTACGATGCTCCATCCT	354
Qy	318	TGTGCTCAACGTCACCTCTGAAAGACTCTGGGCTCTACACCTTGCAATGTGTGCCGGAGTT	377
Db	355	TCCTCTGGAACCTGCAGTTCGACGACAAATGGGACATACACCTGCCAGGTGAAGAACCCACC	414
Qy	378	TGAGTTTGAAGCG	390
Db	415	TGATGTTGATGGG	427

RESULT 12

```

US-10-131-826A-487
; Sequence 487, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 487
; LENGTH: 1371
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-487

```

Qy	198	CGAGGGCGGTAAAGATTTCCTATTATTACAGTATCGGAATGGCCACCGAGGAGTGGAGAG	257
Db	327	CGGGGACCTGAGCAGTTGTATTCTACTACACATAGATCCCTTCCAAACCCATGAGTGG	386
Qy	258	CCCCTTTTCAGGGCGCCTGCAAGTGGAAATGGCAGCAAGGACCTGCAGGACGTGTCATCAC	317
Db	387	GCAGTTTAAAGAACCGGTGTCTTGGGATGGGAATCCTGAGCGGTACGATGCCTTCATCCT	446
Qy	318	TGTGCTCAACGCTCACTCTGAAACGACTCTGGGCTCTACACCTGCAATGTGTCCGGGAGTT	377
Db	447	TCTCTGGAACATGCAGTTCGAGTTCGACGACAAATGGGCATACACCTGCCAGGTGMAAGAACCCACC	506
Qy	378	TGAGTTTGAGGCG	390
Db	507	TGATGTTGATGGG	519

RESULT 13

```

US-10-131-826A-371
; Sequence 371, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIORITY FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 371
; LENGTH: 2849
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-371

```

Query Match 5.6%; Score 36.2; DB 6; Length 1371;
Best Local Similarity 49.2%; Pred. No. 0.39;
Matches 95; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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; Best Local Similarity 47.9%; Pred. No. 0.89;
Matches 102; Conservative 0; Mismatches 111; Indels 0; Gaps 0;
Qy 105 CGTCAGGGCAACCCCATGAAGCTGCGCTGCATCTCTGCAATGAAGAGAGGAGGTGGA 164
Db 898 CGTCACACCTGGAAACCAAGAGGAGACCTACCTGCACATCATGAAGAACGAGGAGGAGT 957
Qy 165 GGCACACACGCTGGTGGGAATGGTTCTACAGGCCCGAGGGCGTAAAGATTTCCTTATTTA 224
Db 958 GGTGATCTTGTTCGCGAGGTGGGGACCGCAGCATATGCAAAAGCCAGACCTGATGCT 1017
Qy 225 CGAGTATCGGAATGGCCACAGGAGGTGGAGAGCCCTTTTCAGGGGCGCCTGCGATGGAA 284
Db 1018 GGAGCTCGAGAGCAGGACCAAGGTGGTGGTACGCTCTTACAAGGCGCAACGTGAGAACGC 1077
Qy 285 TGGCAGCAGACCTGCGAGGAGCTGTCCATCAC 317
Db 1078 CATCTTCAGCGAGGAGCTGGACACCTACATCAC 1110
```

RESULT 14

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US-11-121-086-21
; Sequence 21, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138-6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; PRIOR FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 175100
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-21
```

```
Query Match 5.2%; Score 34; DB 7; Length 175100;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 70; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
Qy 43 CTTATCTACTGGTCAAGTGTCTGCTTCCCTGTGTGTGTGGAGTCCCTCGGAGACGGAG 102
Db 81718 CTGGTGTGCTGATCAGTGACTTCTACCCGGGAGCTGTGAAAGTGGCCCTGGAAGGCAGAT 81777
Qy 103 GCGGTGCAGGGCAACCCCATGAAGCTGCGCTGCATCTCTGCATGAAGAGAGAGGAGTG 162
Db 81778 GGCAGCCCGTCAACGCGGGAGTGGAGACCACACCTCTCAACACAGAGCAACACAG 81837
Qy 163 GAGGCCACCA 172
Db 81838 TACGCGGCCA 81847
```

RESULT 15

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US-10-750-185-61749
; Sequence 61749, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
```

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; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61749
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Bovine 19866881469933
US-10-750-185-61749

Query Match 5.2%; Score 33.8; DB 6; Length 1485;
Best Local Similarity 50.3%; Pred. No. 2;
Matches 83; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
Qy 462 CTCTGTGGTCTCAGAAATCATGATGATACATCTTCTGTGTTCTTCTACCCCTGTGGCTGCT 521
Db 1291 CTCTGGTAAACAATGGAAAAATGATGTTCATCCAAAGACATCTCCCTTTCTTACTGAA 1350
Qy 522 CATCGAGATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAAAGGAGCGAGCCCAAGAAAA 581
Db 1351 GCTCAGATAGAAAAATTTTACACCTTGGTAAACAGAGGCGCAGCTGGACAGAGAGAAAA 1410
Qy 582 CGCGTCTGACTACCTTGGCCATCCCATCTGAGAAACAAGGAGAACTC 626
Db 1411 AGCCGAGTACAACATCATCACCATCACGGGCACTGACATGGGAACCC 1455
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Search completed: December 13, 2005, 14:42:59
Job time : 176.718 secs

Result No.	Score	Query			ID	Description
		Match	Length	DB		
C 1	38.6	16.2	6242	3	US-09-949-016-16490	Sequence 16490, A
C 2	37.8	15.9	14566	3	US-09-949-016-16765	Sequence 16765, A
C 3	37.2	15.6	23640	3	US-09-949-016-13646	Sequence 13646, A
C 4	37	15.5	767677	3	US-09-949-016-12147	Sequence 12147, A
C 5	37	15.5	767677	3	US-09-949-016-17361	Sequence 17361, A
C 6	36.2	15.2	7218	2	US-08-232-463-14	Sequence 14, A
C 7	36.2	15.2	60276	3	US-09-949-016-15004	Sequence 15004, A
C 8	36.2	15.2	60338	3	US-09-949-016-15694	Sequence 15694, A
C 9	36	15.1	232820	3	US-09-949-016-14139	Sequence 14139, A
C 10	35.8	15.0	71278	3	US-09-949-016-11851	Sequence 11851, A
C 11	35.8	15.0	71278	3	US-09-949-016-17563	Sequence 17563, A
C 12	35.8	15.0	168174	3	US-10-071-411A-63	Sequence 63, A
C 13	35.8	15.0	168273	3	US-10-071-411A-2	Sequence 2, A
C 14	35.4	14.9	601	3	US-09-949-016-74297	Sequence 74297, A
C 15	35.4	14.9	601	3	US-09-949-016-74298	Sequence 74298, A
C 16	35.4	14.9	30656	3	US-09-949-016-14613	Sequence 14613, A
C 17	35.4	14.9	84761	3	US-09-949-016-11919	Sequence 11919, A
C 18	35.4	14.8	84763	3	US-09-949-016-13914	Sequence 13914, A
C 19	35.2	14.8	2482	3	US-10-104-047-520	Sequence 520, A
C 20	35.2	14.8	18900	3	US-09-949-016-16589	Sequence 16589, A
C 21	35.2	14.8	30000	3	US-10-007-010-10	Sequence 10, A
C 22	35.2	14.8	53562	3	US-09-949-016-16286	Sequence 16286, A
C 23	34.4	14.5	601	3	US-09-949-016-79198	Sequence 79198, A
C 24	34.4	14.5	601	3	US-09-949-016-91783	Sequence 91783, A

```
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16765
; LENGTH: 14566
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16765

Query Match          15.9%; Score 37.8; DB 3; Length 14566;
Best Local Similarity 60.0%; Pred. No. 0.037;
Matches 63; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 105 CTTCCCTTCATGCATCCATTGTTCTGTTCAATTCATTCATCATCCACCTGCTCTG 164
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 528 CATCCCTCCATTCATCCATCCACCATCCCTCATTCATTCATTCATCCCTCCATTC 469
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 165 AGCTTTACCTCTGACTCCCTAACTCCATCAGACCTCTACGCACC 209
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 468 ATCATCCCTCCCTCATCCATCTATTCATCCATCCACCCCATC 424

RESULT 3
US-09-949-016-13646
; Sequence 13646, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13646
; LENGTH: 23640
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)-(23640)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13646

Query Match          15.6%; Score 37.2; DB 3; Length 23640;
Best Local Similarity 65.9%; Pred. No. 0.073;
Matches 54; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 107 TCCCTTCATGCATCCATTGTTCTGTTCAATTCATTCATCCATCCACCTGCTCTGAG 166
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7218 TCCATCCATGCACCCATCCATTCATTCATCCATCCACCATCTTCCACCTATCCATCCA 7277
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 167 CTTTCACCTCTGACTCCCTAAC 188
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7278 CTTATACTTCTACCTACCCATC 7299
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
US-09-949-016-12147/c

; Sequence 12147, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12147
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12147

Query Match          15.5%; Score 37; DB 3; Length 767677;
Best Local Similarity 60.4%; Pred. No. 0.41;
Matches 61; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 109 CCTTCATGCATCCATTCCTGTTCTGTTCAATTCATTCATCCATCCACCTGCTCTGAGCT 168
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 542579 CCTTCCTCATTCATCCATCTCTCCATCCATTCACCCACATCCATCCATCTCTCT 542520
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 169 TTCACCTCTGACTCCCTTAACTCCATCCATCAGACCTCTTACGCACC 209
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 542519 TACATCCATCCACCCATCCATCTCTCTTCATCCATCCATC 542479
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
US-09-949-016-17361/c
; Sequence 17361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17361
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361

Query Match          15.5%; Score 37; DB 3; Length 767677;
Best Local Similarity 60.4%; Pred. No. 0.41;
Matches 61; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
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QY 109 CCTTCATGCATCCATTGTTCTGTTTCATTTCATTCATCATCATCCACCTGCCTCTGAGCT 168
Db 542579 CCTTCCTCCATCCATCCATCCCTCCATCCATCCATCCATCCATCCATCCATCCATCCAT 542520
QY 169 TTCACTCTGACTCCCTAACTCAATCCATCAGACTCTTACGCACC 209
Db 542519 TACATCCATCACCACCATCCATCCCTTCTTCATCCATCCATC 542479

RESULT 6

US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: ptzgt-F16

US-08-232-463-14

Query Match 15.2%; Score 36.2; DB 2; Length 7218;

Best Local Similarity 8.4%; Pred. No. 0.094;

Matches 17; Conservative 109; Mismatches 77; Indels 0; Gaps 0;

QY 20 GAGTGGCCCTGAACACCTGAGGAGCTGAGATCCCATCCATGTTTCAGCAATGTCATGGCATCA 79
Db 1035 GAGCTTGGCTGACGTTGAGGAGCTGCGATATATATATATATATATATATATATATATATAT 1094

QY 80 GGAGGGCGCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 139
Db 1095 YY 1154

QY 140 TCATCCATACATCACTGCTGAGCTTTCATCTGACTTCCTCACTCACTCACTCACTCACTCACTCA 199
Db 1155 YY 1214

QY 200 TTACACGACCATTAAGACTCTGCC 222
Db 1215 YYYYYYYYYYYYYYYYYYYYYY 1237

RESULT 7

US-09-949-016-15004
; Sequence 15004, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15004
; LENGTH: 60276
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(60276)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15004

Query Match 15.2%; Score 36.2; DB 3; Length 60276;

Best Local Similarity 57.5%; Pred. No. 0.25;

Matches 65; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 111 TTTCATGCATCCATTGTTCTGTTTCATTTCATTCATCCATCATCCATCCATCCATCCATCCAT 170
Db 11773 TCATCGATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 11832

QY 171 CACCTCTGACTCCCTAACTCCATCCATCAGACTCTTACGACCATTAAGACTCTGCCA 223
Db 11833 TCACCATCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 11885

RESULT 8

US-09-949-016-15694
; Sequence 15694, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15694
; LENGTH: 60338
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature

```
; LOCATION: (1)...(60338)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15694

Query Match      15.2%; Score 36.2; DB 3; Length 60338;
Best Local Similarity 57.5%; Pred. No. 0.25;
Matches 65; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 111 TTGATGATCCATTTGTTCTGTTTCATTCATCCATACATCCACCTGCTCTGAGCTTT 170
Db 11835 TCCATGATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 11894
Qy 171 CACCTCTGACCTCCCTAACTCCATCCATCAGACCTCTAGCGCACCAATAAGACTCTGCCA 223
Db 11895 TCACCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 11947

RESULT 9
US-09-949-016-14139/c
; Sequence 14139, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14139
; LENGTH: 323820
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(323820)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14139

Query Match      15.1%; Score 36; DB 3; Length 323820;
Best Local Similarity 70.6%; Pred. No. 0.62;
Matches 48; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 89 CCCAAGGCCCGCCATCGTTCCCTTCATCCATCCATCCATCCATCCATCCATCCATCCATA 148
Db 88457 CTCAGGCGCCCTGTTCTCCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATC 88398
Qy 149 CATCCACC 156
Db 88397 CATCCAAC 88390

RESULT 10
US-09-949-016-11851/c
; Sequence 11851, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14139
; LENGTH: 323820
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(323820)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11851/c

Query Match      15.0%; Score 35.8; DB 3; Length 71278;
Best Local Similarity 56.3%; Pred. No. 0.36;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 105 CTTCCTTCATGATCCATTTGTTCTGTTTCATTCATCCATCCATCCATCCATCCATCC 164
Db 40115 CATCCATCCATCTATCCATCCATCCATCTCTGTCTATATCTTCATCCATCCATCCATCC 40056
Qy 165 AGCTTTACCTCTGACTCCCTTAACCTCCATCCAGACCTCTACGCCACCAATAAGACTCTGCCA 223
Db 40055 ACCATCCACCCATCAATCCATCCATCCATCCATCCATCCATCCATCCATCTCACTATCTGTCA 39997

RESULT 11
US-09-949-016-17563/c
; Sequence 17563, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17563
; LENGTH: 71278
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(71278)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17563

Query Match      15.0%; Score 35.8; DB 3; Length 71278;
Best Local Similarity 56.3%; Pred. No. 0.36;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 105 CTTCCTTCATGATCCATTTGTTCTGTTTCATTCATCCATCCATCCATCCATCCATCC 164
Db 40115 CATCCATCCATCTATCCATCCATCCATCTCTGTCTATATCTTCATCCATCCATCCATCC 40056
Qy 165 AGCTTTACCTCTGACTCCCTTAACCTCCATCCAGACCTCTACGCCACCAATAAGACTCTGCCA 223
Db 40055 ACCATCCACCCATCAATCCATCCATCCATCCATCCATCCATCCATCCATCTCACTATCTGTCA 39997

RESULT 12
US-10-071-411A-63
; Sequence 63, Application US/10071411A
```

Patent No. 6797475
GENERAL INFORMATION:
APPLICANT: Glenn Barnes
APPLICANT: Joanne Meyer
TITLE OF INVENTION: Detection of Polymorphisms in the Human
FILE REFERENCE: MRI-021
CURRENT APPLICATION NUMBER: US/10/071,411A
PRIOR FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/267,515
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 60/314,248
PRIOR FILING DATE: 2001-08-21
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 63
LENGTH: 168174
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(168174)
OTHER INFORMATION: n = A,T,C or G
US-10-071-411A-63

Query Match 15.0%; Score 35.8; DB 3; Length 168174;
Best Local Similarity 56.3%; Pred. No. 0.54;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
Qy 105 CTTCCTTCATGCATCCATGTTCTGTTTCATTCATCCATCCACCTGCTG 164
Db 12256 CATCCATCCATCTATCCATCCATCTCTGTTATCTTCCATCCACCATTC 12315
Qy 165 AGCTTTACCTCTGACTCCCTCACTCCATCCATCCAGACTCTACGCCATAGACTCTGCCA 223
Db 12316 ACATCCACCATCAATCCATCCATCCATCCATCCATCCATCCATCTCACTATCTGTCA 12374

RESULT 13
US-10-071-411A-2
Sequence 2, Application US/10071411A
Patent No. 6797475
GENERAL INFORMATION:
APPLICANT: Glenn Barnes
APPLICANT: Joanne Meyer
TITLE OF INVENTION: Detection of Polymorphisms in the Human
FILE REFERENCE: MRI-021
CURRENT APPLICATION NUMBER: US/10/071,411A
PRIOR FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/267,515
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 60/314,248
PRIOR FILING DATE: 2001-08-21
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 168273
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(168273)
OTHER INFORMATION: n = A,T,C or G
US-10-071-411A-2

Query Match 15.0%; Score 35.8; DB 3; Length 168273;
Best Local Similarity 56.3%; Pred. No. 0.54;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
Qy 105 CTTCCTTCATGCATCCATGTTCTGTTTCATTCATCCATCCACCTGCTG 164
Db 12256 CATCCATCCATCTATCCATCCATCTCTGTTATCTTCCATCCACCATTC 12315

Qy 165 AGCTTTACCTCTGACTCCCTAACTCACTCAGACCTCTACGCCATTAAGACTCTGCCA 223
Db 12316 ACCATCCACCCCAATCCATCCATCCATCCATCCATCCATCCATCTCACTATCTGTCA 12374

RESULT 14

US-09-949-016-74297
Sequence 74297, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 74297
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-74297

Query Match 14.9%; Score 35.4; DB 3; Length 601;
Best Local Similarity 63.5%; Pred. No. 0.058;
Matches 54; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 105 CTTCCTTCATGCATCCATGTTCTGTTTCATTCATCCATCCACCTGCTG 164
Db 217 CATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 276
Qy 165 AGCTTTACCTCTGACTCCCTAACT 189
Db 277 AATTTTATTTCTCTCTCTCTCTCT 301

RESULT 15

US-09-949-016-74298
Sequence 74298, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 74298
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-74298

Query Match 14.9%; Score 35.4; DB 3; Length 601;
Best Local Similarity 63.5%; Pred. No. 0.058;
Matches 54; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy	105	CTTCCCTTCATGCATCCATTGTTCTGTTCATTTCATCCATACATCCACCTGCCCTCTG	164
Db	158	CATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC	217
Qy	165	AGCTTTACCTCTGACTCCCTAACT	189
Db	218	AATTTTATTCTCTCTCTCTCT	242

Search completed: December 13, 2005, 07:35:20
Job time : 61.2062 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 07:13:57 ; Search time 271.784 Seconds
(without alignments)
7241.448 Million cell updates/sec

Title: US-09-977-579A-4_COPY_1024_1261
Perfect score: 238
Sequence: 1 aacaggagcagtgtgacatg.....tgcagaaactgagaagccgg 238

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	238	100.0	600	10	US-11-060-756-2816
2	238	100.0	600	10	US-11-060-756-2817
3	238	100.0	600	10	US-11-060-756-7088
4	238	100.0	600	10	US-11-060-756-7089
5	238	100.0	1261	3	US-09-977-579-4
6	238	100.0	1261	9	US-10-482-834A-22
7	216	90.8	4625	3	US-09-764-891-7659
8	87	36.6	495	4	US-09-925-065A-807954
9	87	36.6	502	4	US-09-925-065A-807996
10	86	36.1	495	4	US-09-925-065A-778585
11	40.6	17.1	599	4	US-09-925-065A-252659
12	40.6	17.1	223380	5	US-10-174-014-12
13	40.6	17.1	233380	5	US-10-087-192-652
14	39.2	16.5	623	4	US-09-925-065A-944616
15	39.2	16.5	1702	4	US-09-925-065A-681163
16	39.2	16.5	1702	4	US-09-925-065A-681164
17	38.4	16.1	228	8	US-10-674-124A-21325
18	38	16.0	623	4	US-09-925-065A-917353
19	38	16.0	623	4	US-09-925-065A-944614
20	38	16.0	27079	6	US-10-034-650-55
21	38	16.0	38360	3	US-09-999-121-14
22	37.8	15.9	109	8	US-10-674-124A-4659
23	37.8	15.9	195	8	US-10-674-124A-4658

24	37.8	15.9	634	4	US-09-925-065A-499987	Sequence 499987,
25	37.8	15.9	634	4	US-09-925-065A-499988	Sequence 499988,
26	37.8	15.9	634	4	US-09-925-065A-499989	Sequence 499989,
27	37.8	15.9	634	4	US-09-925-065A-499990	Sequence 499990,
C 28	37.8	15.9	1091	5	US-10-027-632-30772	Sequence 30772, A
C 29	37.8	15.9	1091	6	US-10-027-632-30772	Sequence 30772, A
30	37.8	15.9	1327	5	US-10-027-632-215913	Sequence 215913,
31	37.8	15.9	1327	6	US-10-027-632-215913	Sequence 215913,
C 32	37.8	15.9	2750	4	US-09-925-065A-31066	Sequence 31066, A
C 33	37.8	15.9	2750	4	US-09-925-065A-31067	Sequence 31067, A
C 34	37.8	15.9	3768	3	US-09-969-708-464	Sequence 164, App
C 35	37.8	15.9	3768	3	US-09-954-531-164	Sequence 164, App
C 36	37.8	15.9	3768	3	US-09-954-531-373	Sequence 373, App
C 37	37.8	15.9	3768	3	US-09-960-706-1041	Sequence 1041, App
C 38	37.8	15.9	3768	3	US-09-873-319-689	Sequence 689, App
C 39	37.8	15.9	3768	9	US-10-843-641A-1231	Sequence 1231, Ap
C 40	37.8	15.9	3768	9	US-10-843-641A-1440	Sequence 1440, Ap
C 41	37.8	15.9	3768	9	US-10-843-641A-7935	Sequence 7935, Ap
C 42	37.8	15.9	3768	9	US-10-287-436A-642	Sequence 642, App
C 43	37.8	15.9	8222	9	US-10-486-319A-6	Sequence 6, Appli
C 44	37.8	15.9	8222	9	US-10-486-319A-42	Sequence 42, Appl
C 45	37.8	15.9	8222	9	US-10-486-319A-64	Sequence 64, Appl

ALIGNMENTS

RESULT 1

US-11-060-756-2816
; Sequence 2816, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2816
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2816

Query Match	100.0%;	Score 238;	DB 10;	Length 600;
Best Local Similarity	100.0%;	Pred. No. 1e-68;	Mismatches 0;	Indels 0;
Matches 238;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AACAGGAGCAGTGTGACATGAGTGGCTGAAACACCTGAGGGACTGGACATCCCATGTC	60	
Db	363	AACAGGAGCAGTGTGACATGAGTGGCTGAAACACCTGAGGGACTGGACATCCCATGTC	422	
Qy	61	AGCAATGTCAATGGCATCAGAGGGGGCCCAAGGGCCCATCGCTTCCCTTCATGATC	120	
Db	423	AGCAATGTCAATGGCATCAGAGGGGGCCCAAGGGCCCATCGCTTCCCTTCATGATC	482	
Qy	121	CATTGTCTGTTTCATTTCATTCATCCATACATCCACCTGCTTCTGAGCTTTCACCTCTGAC	180	
Db	483	CATTGTCTGTTTCATTTCATTCATCCATACATCCACCTGCTTCTGAGCTTTCACCTCTGAC	542	
Qy	181	TCCTTAACCTCCATCAGACCTCTAGCACCATAAGACTCTGCCAGAACTGAGAGCCCG	238	
Db	543	TCCTTAACCTCCATCAGACCTCTAGCACCATAAGACTCTGCCAGAACTGAGAGCCCG	600	

RESULT 2

US-11-060-756-2817
; Sequence 2817, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:

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; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2817
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2817

Query Match      100.0%; Score 238; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 1e-68;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACAGGAGCAGTGTGACATGAGGTGGCTGAACACCTGAGGGACTGGACATCCCATGTTTC 60
Db 363 AACAGGAGCAGTGTGACATGAGGTGGCTGAACACCTGAGGGACTGGACATCCCATGTTTC 422

Qy 61 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGCTTCCCTTTCATGCATC 120
Db 423 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGCTTCCCTTTCATGCATC 482

Qy 121 CATTGTTCTGTTCATTCAATTCATCATACATCCACCTGCGCTTCTGAGCTTTTCACTCTGAC 180
Db 483 CATTGTTCTGTTCATTCAATTCATCATACATCCACCTGCGCTTCTGAGCTTTTCACTCTGAC 542

Qy 181 TCCCTAACTCCATCAGACCTCTACGCACCAATAGACTCTGCCAGAACTGAGAGGCCGG 238
Db 543 TCCCTAACTCCATCAGACCTCTACGCACCAATAGACTCTGCCAGAACTGAGAGGCCGG 600

RESULT 3
US-11-060-756-7088
; Sequence 7088, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7088
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7088

Query Match      100.0%; Score 238; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 1e-68;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACAGGAGCAGTGTGACATGAGGTGGCTGAACACCTGAGGGACTGGACATCCCATGTTTC 60
Db 363 AACAGGAGCAGTGTGACATGAGGTGGCTGAACACCTGAGGGACTGGACATCCCATGTTTC 422

Qy 61 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGCTTCCCTTTCATGCATC 120
Db 423 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGCTTCCCTTTCATGCATC 482

Qy 121 CATTGTTCTGTTCATTCAATTCATCATACATCCACCTGCGCTTCTGAGCTTTTCACTCTGAC 180
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Qy 181 TCCCTAACTCCATCAGACCTCTACGCACCAATAGACTCTGCCAGAACTGAGAGGCCGG 238
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; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2817
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2817

Query Match      100.0%; Score 238; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 1e-68;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGCTTCCCTTTCATGCATC 120
Db 423 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGCTTCCCTTTCATGCATC 482

Qy 121 CATTGTTCTGTTCATTCAATTCATCATACATCCACCTGCGCTTCTGAGCTTTTCACTCTGAC 180
Db 483 CATTGTTCTGTTCATTCAATTCATCATACATCCACCTGCGCTTCTGAGCTTTTCACTCTGAC 542

Qy 181 TCCCTAACTCCATCAGACCTCTACGCACCAATAGACTCTGCCAGAACTGAGAGGCCGG 238

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; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7089
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7089

Query Match      100.0%; Score 238; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 1e-68;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACAGGAGCAGTGTGACATGAGGTGGCTGAACACCTGAGGGACTGGACATCCCATGTTTC 60
Db 363 AACAGGAGCAGTGTGACATGAGGTGGCTGAACACCTGAGGGACTGGACATCCCATGTTTC 422

Qy 61 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGCTTCCCTTTCATGCATC 120
Db 423 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGCTTCCCTTTCATGCATC 482

Qy 121 CATTGTTCTGTTCATTCAATTCATCATACATCCACCTGCGCTTCTGAGCTTTTCACTCTGAC 180
Db 483 CATTGTTCTGTTCATTCAATTCATCATACATCCACCTGCGCTTCTGAGCTTTTCACTCTGAC 542

Qy 181 TCCCTAACTCCATCAGACCTCTACGCACCAATAGACTCTGCCAGAACTGAGAGGCCGG 238
Db 543 TCCCTAACTCCATCAGACCTCTACGCACCAATAGACTCTGCCAGAACTGAGAGGCCGG 600

RESULT 5
US-09-977-579-4
; Sequence 4, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
; TITLE OF INVENTION: channel
; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977,579
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-977-579-4

Query Match      100.0%; Score 238; DB 3; Length 1261;
Best Local Similarity 100.0%; Pred. No. 1.3e-66;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 73; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Qy 46 GGACATCCCATGTTTCAGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCCCATGCG 105
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Qy 166 GCTTTCA 172
Db 46167 CTTATCA 46173

RESULT 13
US-10-087-192-652
; Sequence 652, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 652

; NAME/KEY: unsure
; LOCATION: 78004
; OTHER INFORMATION: unknown
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; NAME/KEY: unsure
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Query Match
Best Local Similarity 17.1%; Score 40.6; DB 6; Length 221000;
Matches 73; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Qy 46 GGACATCCCATGTTTCAGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCCCATGCG 105
Db 46047 GGAGCTCCCATGCTGGGGAAGATTCATTTCATTGGGAGCTCCCATGCTGGGAGATCC 46106

Qy 106 TTCCTTCATGCATCCATGTTCTGTTTCATTCATTCATTCATTCATTCATTCATTCATTC 165
Db 46107 ATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 46166

Qy 166 GCTTTCA 172
Db 46167 CTTATCA 46173

RESULT 14
US-09-925-065A-944616
; Sequence 944616, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 944616
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-944616

Query Match
Best Local Similarity 16.5%; Score 39.2; DB 4; Length 623;
Matches 59; Conservative 1; Mismatches 34; Indels 0; Gaps 0;

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Qy 157 TGCTCTGAGCTTTCACCTCTGACTCCCTAATC 190
Db 517 TATCTATCTAGCTACCGAGCTAGCTACCTRTATC 550

RESULT 15
US-09-925-065A-681163/C
; Sequence 681163, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
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1	238	100.0	1261	6	US-10-374-954-8	Sequence 8, Appli
2	37.8	15.9	200628	7	US-11-121-086-62	Sequence 62, Appli
C 3	37.2	15.6	126552	7	US-11-121-086-1	Sequence 1, Appli
C 4	37.2	15.6	162173	7	US-11-121-086-72	Sequence 72, Appli
C 5	36.6	15.4	181172	7	US-11-121-086-41	Sequence 41, Appli
6	36	15.1	162537	7	US-11-121-086-59	Sequence 59, Appli
C 7	34.6	14.5	169725	7	US-11-121-086-63	Sequence 63, Appli
8	34.2	14.4	1408	6	US-10-750-185-50889	Sequence 50889, A
C 9	33.6	14.1	119160	7	US-11-121-086-12	Sequence 12, Appli
C 10	32.8	13.8	150468	7	US-11-112-908-56	Sequence 56, Appli
C 11	32.8	13.8	169495	7	US-11-121-086-61	Sequence 61, Appli
12	32.8	13.8	193789	7	US-11-112-908-55	Sequence 55, Appli
C 13	32.8	13.8	207908	7	US-11-112-908-21	Sequence 21, Appli
C 14	32.8	13.8	212805	7	US-11-112-908-19	Sequence 19, Appli
C 15	32.6	13.7	200628	7	US-11-121-086-62	Sequence 62, Appli
C 16	32.4	13.6	148220	7	US-11-121-086-90	Sequence 90, Appli
17	32.2	13.5	126552	7	US-11-121-086-1	Sequence 1, Appli
18	32.2	13.5	191684	7	US-11-121-086-2	Sequence 2, Appli
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20	32	13.4	119160	7	US-11-121-086-12	Sequence 12, Appli
21	31.8	13.4	172111	7	US-11-121-086-28	Sequence 28, Appli
22	31.4	13.2	1532	6	US-10-750-185-42215	Sequence 42215, A
23	31.4	13.2	1888	6	US-10-750-185-47114	Sequence 47114, A

Query Match	14.4%	Score 34.2;	DB 6;	Length 1408;
Best Local Similarity	71.4%;	Pred. No. 0.057;		
Matches 45;	Conservative	0;	Mismatches 18;	Indels 0;
Gaps	0;			

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Db	686	TCCATCCCTCCATTTCATCGATCCATTCATTCATTCATTCATCCATCCACCATCCACCCAC	745
Qy	167	CTT	169
Db	746	ATT	748

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RESULT 9
US-11-121-086-12/c
; Sequence 12, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIEUSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 119160
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-12

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	Query Match	14.1%	Score 33.6	DB 7	Length 119160	
	Best Local Similarity	63.8%	Pred No. 0	53		
	Matches 51	Conservative 0	Mismatches 29	Indels 0	Gaps 0	
Qy	102	TGCTTCCCTTCATGCATCCATTGTTCTGTTTCATTCATTCATCATCATCCACCTGCCT	161			
Db	19829	TCTTTTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATCA	17770			
Qy	162	CTGAGCTTTTCACCTCTGACT	181			
Db	19769	CTCATTCCTCTGCTATGCT	19750			

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RESULT 10
US-11-112-908-56
; Sequence 56, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
;
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE OF INVENTION: 04-164-US
; CURRENT APPLICATION NUMBER: US-11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 07:35:31 ; Search time 260 Seconds
(without alignments)
8621.174 Million cell updates/sec

Title: US-09-977-579A-4

Perfect score: 1261

Sequence: 1 cccctccctccgagctgagc.....tgccagaactgagaagccgg 1261

Scoring table: OLIGO NUC

Gapop 60.0, Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 10

Total number of hits satisfying chosen parameters: 638931

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/1_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	24	1.9	601	3	US-09-949-016-26733
C 2	24	1.9	601	3	US-09-949-016-194175
C 3	24	1.9	137949	3	US-09-949-016-12196
C 4	24	1.9	137956	3	US-09-949-016-17260
C 5	20	1.6	1491	3	US-09-902-540-6997
C 6	20	1.6	2517	3	US-09-712-363-4
C 7	20	1.6	4312	3	US-09-902-540-612
C 8	20	1.6	4403765	3	US-09-103-840A-2
C 9	20	1.6	4411529	3	US-09-103-840A-1
C 10	19	1.5	601	3	US-09-949-016-85015
C 11	19	1.5	601	3	US-09-949-016-85166
C 12	19	1.5	1626	2	US-08-381-433A-3
C 13	19	1.5	1626	3	US-09-799-978-17
C 14	19	1.5	1626	3	US-09-881-401-3
C 15	19	1.5	5895	3	US-09-902-540-792
C 16	19	1.5	109159	3	US-09-949-016-14169
C 17	19	1.5	109159	3	US-09-949-016-14170
C 18	18	1.4	344	3	US-09-157-177-128
C 19	18	1.4	344	3	US-09-541-210-128
C 20	18	1.4	466	3	US-09-280-116-14
C 21	18	1.4	570	3	US-09-621-976-1635
C 22	18	1.4	601	3	US-09-949-016-56070
C 23	18	1.4	601	3	US-09-949-016-122006
C 24	18	1.4	601	3	US-09-949-016-131295

ALIGNMENTS

RESULT 1

US-09-949-016-26733/c
; Sequence 26733, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26733
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-26733

Query Match 1.9%; Score 24; DB 3; Length 601;
Best Local Similarity 100.0%; Pred No. 0.15; Mismatches 0; Indels 0; Gaps 0;

QY 1156 CATTTCATTCATCATCCACC 1179

Db 472 CATTTCATTCATCATCCACC 449

RESULT 2

US-09-949-016-194175/c
; Sequence 194175, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194175
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
US-09-949-016-194175

Query Match          1.9%; Score 24; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1156 CATTTCATTCATCCATACATCCACC 1179
Db 472 CATTTCATTCATCCATACATCCACC 449

RESULT 3
US-09-949-016-12196
; Sequence 12196, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12196
; LENGTH: 137949
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(137949)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12196

Query Match          1.9%; Score 24; DB 3; Length 137949;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1156 CATTTCATTCATCCATACATCCACC 1179
Db 130759 CATTTCATTCATCCATACATCCACC 130782

RESULT 4
US-09-949-016-17260
; Sequence 17260, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17260
; LENGTH: 137956
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(137956)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17260

Query Match          1.9%; Score 24; DB 3; Length 137956;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1156 CATTTCATTCATCCATACATCCACC 1179
Db 130759 CATTTCATTCATCCATACATCCACC 130782

RESULT 5
US-09-902-540-6997
; Sequence 6997, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6997
; LENGTH: 1491
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-6997

Query Match          1.6%; Score 20; DB 3; Length 1491;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 665 GCAAGGACCTGCAGGACGTG 684
Db 1205 GCAAGGACCTGCAGGACGTG 1224

RESULT 6
US-09-712-363-4/c
; Sequence 4, Application US/09712363
; Patent No. 6892139
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
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; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2517
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; US-09-712-363-4

Query Match      1.6%; Score 20; DB 3; Length 2517;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      500 AGCTGCGCTGCATCTCTGTC 519
Db      82 AGCTGCGCTGCATCTCTGTC 63

RESULT 7
US-09-902-540-612/c
; Sequence 612, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 612
; LENGTH: 4312
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-612

Query Match      1.6%; Score 20; DB 3; Length 4312;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      665 GCAAGGACCTGCAGGACGTG 684
Db      291 GCAAGGACCTGCAGGACGTG 272

RESULT 8
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
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; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
; US-09-103-840A-2

Query Match      1.6%; Score 20; DB 3; Length 4403765;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      500 AGCTGCGCTGCATCTCTGTC 519
Db      7383 AGCTGCGCTGCATCTCTGTC 7364

RESULT 9
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
; US-09-103-840A-1

Query Match      1.6%; Score 20; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      500 AGCTGCGCTGCATCTCTGTC 519
Db      7383 AGCTGCGCTGCATCTCTGTC 7364

RESULT 10
US-09-949-016-85015
; Sequence 85015, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85015
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-85015

Query Match          1.5%; Score 19; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1152 TGTTCATTCATTCATCCAT 1170
Db 465 TGTTCATTCATTCATCCAT 483

RESULT 11
US-09-949-016-85166
; Sequence 85166, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85166
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-85166

Query Match          1.5%; Score 19; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1152 TGTTCATTCATTCATCCAT 1170
Db 465 TGTTCATTCATTCATCCAT 483

RESULT 12
US-08-381-433A-3
; Sequence 3, Application US/08381433A
; Patent No. 5786203
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy W.
; APPLICANT: Oltersdorff, Tilman
; APPLICANT: Liaw, Chen
; APPLICANT: Grigoriadis, Dimitri E.
; APPLICANT: DeSouza, Errol B.
; TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2
; TITLE OF INVENTION: RECEPTORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,433A
; FILING DATE: 31-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 890068.401C1
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANDBERRY
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 216..1449
; US-08-381-433A-3

Query Match          1.5%; Score 19; DB 2; Length 1626;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 CCGGGGTGGCGGGGAGGC 90
Db 95 CCGGGGTGGCGGGGAGGC 113

RESULT 13
US-09-799-978-17
; Sequence 17, Application US/09799978
; Patent No. 6670140
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (216)..(1451)
US-09-799-978-17

Query Match          1.5%; Score 19; DB 3; Length 1626;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 CCGGGGTGGCGGGGAGGC 90
Db 95 CCGGGGTGGCGGGGAGGC 113

RESULT 14
US-09-881-401-3
; Sequence 3, Application US/09881401
; Patent No. 6723841
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy W.
```

; Oltersdorf, Tilman
; Liaw, Chen
; Grigoriadis, Dimitri E.
; Chalmers, Derek T.
; DeSouza, Erol B.
; TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2
; RECEPTORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/881,401
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 690068.401C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 216..1449
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-881-401-3

Query Match 1.5%; Score 19; DB 3; Length 1626;
Best Local Similarity 100.0%; Pred.No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 CCGGGGTGGCGGGGAGGC 90
Db 95 CCGGGGTGGCGGGGAGGC 113
|||||

RESULT 15
US-09-902-540-792
; Sequence 792, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 792
; LENGTH: 5895
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-792

Query Match 1.5%; Score 19; DB 3; Length 5895;
Best Local Similarity 100.0%; Pred.No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 576 GGGCGGTAAGATTTCCTT 594
Db 5033 GGGCGGTAAGATTTCCTT 5051
|||||

Search completed: December 13, 2005, 14:47:33
Job time : 279 secs

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 14:31:47 ; Search time 1161 Seconds
(without alignments)
8981.641 Million cell updates/sec

Title: US-09-977-579A-4
Perfect score: 1261
Sequence: 1 cctctccttcgagctgagc.....tgcagaactgagaagccgg 1261

Scoring table: OLIGO NUC
Gapop 60.0, Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size: 10

Total number of hits satisfying chosen parameters: 4450127

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA Main:*

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- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1261	100.0	1261	3	US-09-977-579-4
2	1210	96.0	1261	9	US-10-482-834A-22
3	600	47.6	600	10	US-11-060-756-2816
4	600	47.6	600	10	US-11-060-756-2817
5	600	47.6	600	10	US-11-060-756-7088
6	600	47.6	600	10	US-11-060-756-7089
7	396	31.4	1195	9	US-10-450-763-22568
8	391	31.0	3531	9	US-10-450-763-22567
9	386	30.6	651	4	US-09-925-065A-513769
10	335	26.6	651	4	US-09-925-065A-513767
11	335	26.6	651	4	US-09-925-065A-513768
12	218	17.3	545	4	US-09-925-065A-774904
13	218	17.3	621	9	US-10-450-763-22566
14	216	17.1	4625	3	US-09-764-891-7659
15	91	7.2	407	7	US-10-276-774-718
16	87	6.9	496	4	US-09-925-065A-807954
17	87	6.9	502	4	US-09-925-065A-807996
18	86	6.8	495	4	US-09-925-065A-778585
19	44	3.5	53	9	US-10-491-192-5
20	44	3.5	60	9	US-10-491-192-6
21	42	3.3	642	4	US-09-925-065A-322798
22	42	3.3	642	4	US-09-925-065A-322799
23	38	3.0	645	5	US-10-029-191-21

24	38	3.0	2220	3	US-09-977-579-3	Sequence 3, Appli
25	38	3.0	2632	5	US-10-029-191-22	Sequence 22, Appli
26	38	3.0	3108	5	US-10-029-191-1	Sequence 1, Appli
27	33	2.6	574	3	US-09-764-891-1293	Sequence 1293, Ap
28	25	2.0	25	10	US-11-060-756-54798	Sequence 54798, A
29	25	2.0	25	10	US-11-060-756-54799	Sequence 54799, A
30	25	2.0	25	10	US-11-060-756-54800	Sequence 54800, A
31	25	2.0	25	10	US-11-060-756-54801	Sequence 54801, A
32	25	2.0	25	10	US-11-060-756-54802	Sequence 54802, A
33	25	2.0	25	10	US-11-060-756-54803	Sequence 54803, A
34	25	2.0	25	10	US-11-060-756-54804	Sequence 54804, A
35	25	2.0	25	10	US-11-060-756-54805	Sequence 54805, A
36	25	2.0	25	10	US-11-060-756-54806	Sequence 54806, A
37	25	2.0	25	10	US-11-060-756-54807	Sequence 54807, A
38	25	2.0	25	10	US-11-060-756-54808	Sequence 54808, A
39	25	2.0	25	10	US-11-060-756-54809	Sequence 54809, A
40	25	2.0	25	10	US-11-060-756-54810	Sequence 54810, A
41	25	2.0	25	10	US-11-060-756-54811	Sequence 54811, A
42	25	2.0	25	10	US-11-060-756-54812	Sequence 54812, A
43	25	2.0	25	10	US-11-060-756-54813	Sequence 54813, A
44	25	2.0	25	10	US-11-060-756-54814	Sequence 54814, A
45	25	2.0	25	10	US-11-060-756-54815	Sequence 54815, A

ALIGNMENTS

RESULT 1
US-09-977-579-4
; Sequence 4, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
; TITLE OF INVENTION: channel
; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977,579
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-977-579-4

Query Match	100.0%;	Score 1261;	DB 3;	Length 1261;
Best Local Similarity	100.0%;	Pred. No. 0;		
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			Indels	0;
			Gaps	0;
Qy	1	CCCTCCCTCCGAGCTGAGCTTACCTCTGGCGCAACAGCAGCGAGCGGCGCGAGTGG	60	
Db	1	CCCTCCCTCCGAGCTGAGCTTACCTCTGGCGCAACAGCAGCGAGCGGCGCGAGTGG	60	
Qy	61	AAGCTGAGTTCCGGGTGGCGGGGAGGCGACTGTCCTGCTGAGCGCGCGCGAGA	120	
Db	61	AAGCTGAGTTCCGGGTGGCGGGGAGGCGACTGTCCTGCTGAGCGCGCGCGAGA	120	
Qy	121	GCGGCGCGAGCGGCTGATCGGCTCCCTGAACTGGGGAGGTCCTGAGTGGGTGCTTAG	180	
Db	121	GCGGCGCGAGCGGCTGATCGGCTCCCTGAACTGGGGAGGTCCTGAGTGGGTGCTTAG	180	
Qy	181	GGCCCAAGCCCAACCCCGGCTCCAAAGCTCCCAAGGCTCCCAAGGCTCCCAAGGCTCCG	240	
Db	181	GGCCCAAGCCCAACCCCGGCTCCAAAGCTCCCAAGGCTCCCAAGGCTCCCAAGGCTCCG	240	
Qy	241	GCCTTCCTTCGCTCAGAAAGTGCCTCCCTGGGGGAGTTCGTCCTCCAAAGGTTCTCTCG	300	

Db 241 GCCCTTCCTTCGGTCAGAAAGTCGCCCTTCGGGGCAGTTCGTCCCAAAGGTTTCCTCG 300
Qy 301 AAAGAACTGAGAGGGCCAGTCTCTTGACCGAGGGAATCTCTCTGTGTAGCCTTGGAGC 360
Db 301 AAAGAACTGAGAGGGCCAGTCTCTTGACCGAGGGAATCTCTCTGTGTAGCCTTGGAGC 360
Qy 361 CGCAGAGCCCAAGAGATGCCCTTCAATAGATTGTTTCCCTCGGCTTCTCTCGTGCTT 420
Db 361 CGCAGAGCCCAAGAGATGCCCTTCAATAGATTGTTTCCCTCGGCTTCTCTCGTGCTT 420
Qy 421 ATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAAAGTGCCTTCGAGACGAGGCC 480
Db 421 ATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAAAGTGCCTTCGAGACGAGGCC 480
Qy 481 GTGACGGGCAACCCCATGAAGTGGCTGCAATCTCTGTCATGAAGAGAGAGGAGTGAG 540
Db 481 GTGACGGGCAACCCCATGAAGTGGCTGCAATCTCTGTCATGAAGAGAGAGGAGTGAG 540
Qy 541 GCCACACGGTGGTGAATGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTAC 600
Db 541 GCCACACGGTGGTGAATGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTAC 600
Qy 601 GAGTATCGGAATGGCCACGAGAGTGAGAGGCCCTTTTCAGGGGCGCTCGAGTGAAT 660
Db 601 GAGTATCGGAATGGCCACGAGAGTGAGAGGCCCTTTTCAGGGGCGCTCGAGTGAAT 660
Qy 661 GGCAGCAAGGACCTCGAGAGGTGTCATCTACTGTGTCACGTCACGTCTGAAAGACTCT 720
Db 661 GGCAGCAAGGACCTCGAGAGGTGTCATCTACTGTGTCACGTCACGTCTGAAAGACTCT 720
Qy 721 GGCCTCTACACTGCAATGTGTCGGGAGTTTGAAGTTGAGGGGCATCGGCCCTTTGTG 780
Db 721 GGCCTCTACACTGCAATGTGTCGGGAGTTTGAAGTTGAGGGGCATCGGCCCTTTGTG 780
Qy 781 AAGACGACGGGCTGATCCCCCTAAGAGTCAACGAGAGGAGTGGAGAGACTTCACCTCT 840
Db 781 AAGACGACGGGCTGATCCCCCTAAGAGTCAACGAGAGGAGTGGAGAGACTTCACCTCT 840
Qy 841 GTGGTCTCAGAAATCATGATGATACATCTTCTGTGTCCTCACCTGTGGTGTCTATC 900
Db 841 GTGGTCTCAGAAATCATGATGATACATCTTCTGTGTCCTCACCTGTGGTGTCTATC 900
Qy 901 GAGATGATATATGCTACAGAAAGTCTCAAAAGCCGAGAGGAGCCCAAGAAACCGG 960
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Qy 961 TCTGACTACCTTGCCATCCCATCTCAGAAACAGAGAACTCTGCGGTACCAAGTGGAGAA 1020
Db 961 TCTGACTACCTTGCCATCCCATCTCAGAAACAGAGAACTCTGCGGTACCAAGTGGAGAA 1020
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Db 1021 TAGAACAGAGCAGTGTGACATGAGTGGCTGTGAACACCTGAGGAGCTGGACATCCCATG 1080
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Qy 1141 ATCCCATTTGTTGTTCAATTCATTCATATCATATCATCCACCTGCTCTGAGCTTTCACCTCT 1200
Db 1141 ATCCCATTTGTTGTTCAATTCATTCATATCATATCATCCACCTGCTCTGAGCTTTCACCTCT 1200
Qy 1201 GACTCCCTAACTCCATCAGACTCTTACGCAACATTAAGACTGTGGCAGAACTGAGAAGCGG 1260
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Qy 1261 G 1261
Db 1261 G 1261

; Sequence 22, Application US/10482834A
; Publication No. US20050074764A1
; GENERAL INFORMATION: John Charles
; APPLICANT: Mulley, John Charles
; APPLICANT: Harkin, Louise Anne
; APPLICANT: Dibbens, Michelle
; APPLICANT: Wallace, Robyn
; APPLICANT: Phillips, Hilary Anny
; APPLICANT: Heron, Sara Elizabeth
; APPLICANT: Berkovic, Samuel Frank
; APPLICANT: Scheffer, Ingrid Eileen
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
; FILE REFERENCE: 1386/17
; CURRENT APPLICATION NUMBER: US/10/482,834A
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-482-834A-22

Query Match 96.0%; Score 1210; DB 9; Length 1261;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTCCCTTCGAGCTGAGCTTACCCTGGGCGCAAAAGAGCGAGGCGGAGTGG 60
Db 1 CCCTCCCTTCGAGCTGAGCTTACCCTGGGCGCAAAAGAGCGAGGCGGAGTGG 60
Qy 61 AAGTGAAGTCCCGGTGGCGGGAGGAGCTGTCGTTGGTGTGAGCCCGCGAGA 120
Db 61 AAGTGAAGTCCCGGTGGCGGGAGGAGCTGTCGTTGGTGTGAGCCCGCGAGA 120
Qy 121 GCGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGGTGCCTTAG 180
Db 121 GCGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGGTGCCTTAG 180
Qy 181 GGGCCAAAGCCCCCAGCCGGCTCCAAAGTCTCCAGGGCTCCCGAGGCAACGGTGTCTG 240
Db 181 GGGCCAAAGCCCCCAGCCGGCTCCAAAGTCTCCAGGGCTCCCGAGGCAACGGTGTCTG 240
Qy 241 GCGCTTCCTCGGTGAGAAAGTCCGCTCCCGGCGAGTTCGTCCCAAGGGTTCCTCG 300
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Qy 361 CGCAGAGCCCAAGAGATGCCCTTCAATAGATTGTTTCCCTCGGCTTCTCTCGTGCTT 420
Db 361 CGCAGAGCCCAAGAGATGCCCTTCAATAGATTGTTTCCCTCGGCTTCTCTCGTGCTT 420
Qy 421 ATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAAAGTGCCTTCGAGACGAGGCC 480
Db 421 ATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAAAGTGCCTTCGAGACGAGGCC 480
Qy 481 GTGACGGGCAACCCCATGAAGTGGCTGCAATCTCTGTCATGAAGAGAGAGGAGTGAG 540
Db 481 GTGACGGGCAACCCCATGAAGTGGCTGCAATCTCTGTCATGAAGAGAGAGGAGTGAG 540
Qy 541 GCCACACGGTGGTGAATGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTAC 600
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Qy 661 GGCAGCAAGGACCTCGAGAGGTGTCATCTACTGTGTCACGTCACGTCTGAAAGACTCT 720


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Qy 962 CTGACTACCTTGGCCATCCCATCTCAGAACCAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 1021
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Qy 1022 AGAACAGGAGCAGTGTGACATGAGTGGCCCTGGAACACCTGAGGGACTGGACATCCCATGT 1081
Db 361 AGAACAGGAGCAGTGTGACATGAGTGGCCCTGGAACACCTGAGGGACTGGACATCCCATGT 420
Qy 1082 TCAGCAATGTCAATGGCAATCAGAGAGGCGGCCCAAGGGCCCCCAAGGGCCCCATCGCTTCCCTTTCATGCA 1141
Db 421 TCAGCAATGTCAATGGCAATCAGAGAGGCGGCCCAAGGGCCCCCAAGGGCCCCATCGCTTCCCTTTCATGCA 480
Qy 1142 TCCATTGTTCTGTTCAATTCATCCATACATCCACTGCTGCTGAGCTTTCACCTCTG 1201
Db 481 TCCATTGTTCTGTTCAATTCATCCATACATCCACTGCTGCTGAGCTTTCACCTCTG 540
Qy 1202 ACTCCCTAACTCCATCAGACCTCTACGCACCATAGACTCTGCCAGAACTGAGAAGCGG 1261
Db 541 ACTCCCTAACTCCATCAGACCTCTACGCACCATAGACTCTGCCAGAACTGAGAAGCGG 600

RESULT 5
US-11-060-756-7088
; Sequence 7088, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7088
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7088
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 662 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAAGCTCACTCTGAACGACTCTG 721
Db 1 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAAGCTCACTCTGAACGACTCTG 60

Qy 722 GCCTCTACACCTGCAATGTGTCCCGGAGTTTGAAGTTCAGGCGCATCGGCCCTTTGTGA 781
Db 61 GCCTCTACACCTGCAATGTGTCCCGGAGTTTGAAGTTCAGGCGCATCGGCCCTTTGTGA 120

Qy 782 AGACGACCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACTCTG 841
Db 121 AGACGACCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACTCTG 180

Qy 842 TGGTCTCAGAAATCATGATGTACATCTTCTGCTTCCCTCACCTGTGGCTGCTCATCG 901
Db 181 TGGTCTCAGAAATCATGATGTACATCTTCTGCTTCCCTCACCTGTGGCTGCTCATCG 240

Qy 902 AGATGATATATTGCTACGAAAGGTCTCAAAGCCGAGAGGCGAGCCCAAGAAACCGGT 961
Db 241 AGATGATATATTGCTACGAAAGGTCTCAAAGCCGAGAGGCGAGCCCAAGAAACCGGT 300

Qy 962 CTGACTACCTTGGCCATCCCATCTCAGAACCAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 1021
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Db 301 CTGACTACCTTGGCCATCCCATCTCAGAACCAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 360
Qy 1022 AGAACAGGAGCAGTGTGACATGAGTGGCCCTGGAACACCTGAGGGACTGGACATCCCATGT 1081
Db 361 AGAACAGGAGCAGTGTGACATGAGTGGCCCTGGAACACCTGAGGGACTGGACATCCCATGT 420
Qy 1082 TCAGCAATGTCAATGGCAATCAGAGAGGCGGCCCAAGGGCCCCCAAGGGCCCCATCGCTTCCCTTTCATGCA 1141
Db 421 TCAGCAATGTCAATGGCAATCAGAGAGGCGGCCCAAGGGCCCCCAAGGGCCCCATCGCTTCCCTTTCATGCA 480
Qy 1142 TCCATTGTTCTGTTCAATTCATCCATACATCCACTGCTGCTTGAAGCTTTCACCTCTG 1201
Db 481 TCCATTGTTCTGTTCAATTCATCCATACATCCACTGCTGCTTGAAGCTTTCACCTCTG 540
Qy 1202 ACTCCCTAACTCCATCAGACCTCTACGCACCATAGACTCTGCCAGAACTGAGAAGCGG 1261
Db 541 ACTCCCTAACTCCATCAGACCTCTACGCACCATAGACTCTGCCAGAACTGAGAAGCGG 600

RESULT 6
US-11-060-756-7089
; Sequence 7089, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7089
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7089
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Query Match 47.6%; Score 600; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 662 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAAGCTCACTCTGAACGACTCTG 721
Db 1 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAAGCTCACTCTGAACGACTCTG 60

Qy 722 GCCTCTACACCTGCAATGTGTCCCGGAGTTTGAAGTTCAGGCGCATCGGCCCTTTGTGA 781
Db 61 GCCTCTACACCTGCAATGTGTCCCGGAGTTTGAAGTTCAGGCGCATCGGCCCTTTGTGA 120

Qy 782 AGACGACCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACTCTG 841
Db 121 AGACGACCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACTCTG 180

Qy 842 TGGTCTCAGAAATCATGATGTACATCTTCTGCTTCCCTCACCTGTGGCTGCTCATCG 901
Db 181 TGGTCTCAGAAATCATGATGTACATCTTCTGCTTCCCTCACCTGTGGCTGCTCATCG 240

Qy 902 AGATGATATATTGCTACGAAAGGTCTCAAAGCCGAGAGGCGAGCCCAAGAAACCGGT 961
Db 241 AGATGATATATTGCTACGAAAGGTCTCAAAGCCGAGAGGCGAGCCCAAGAAACCGGT 300

Qy 962 CTGACTACCTTGGCCATCCCATCTCAGAACCAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 1021
Db 301 CTGACTACCTTGGCCATCCCATCTCAGAACCAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 360

Qy 1022 AGAACAGGAGCAGTGTGACATGAGTGGCCCTGGAACACCTGAGGGACTGGACATCCCATGT 1081
Db 361 AGAACAGGAGCAGTGTGACATGAGTGGCCCTGGAACACCTGAGGGACTGGACATCCCATGT 420

Qy 1082 TCAGCAATGTCAATGGCAATCAGAGAGGCGGCCCAAGGGCCCCCAAGGGCCCCATCGCTTCCCTTTCATGCA 1141
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Matches	385;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	45	GCAGGGCGCGAGTGGAGATTCGAGATTCCGGGGTGGCGGGAGGCGACACTGTCGGTGGTG	104						
Db	172	GCAGGGCGCGAGTGGAGATTCGAGATTCCGGGGTGGCGGGAGGCGACACTGTCGGTGGTG	231						
Qy	105	CTGAGCCCGCGAGAGCGGGCGGAGCGGCTCATCGGCTCCCTCGAACTCGGGGAGGTC	164						
Db	232	CTGAGCCCGCGAGAGCGGGCGGAGCGGCTCATCGGCTCCCTCGAACTCGGGGAGGTC	291						
Qy	165	CAGTGGGGTGGCTTAGGGCCCAAGCCCCCAACCGGGTCCAAAAGCTCCCAAGGGCGCTCCC	224						
Db	292	CAGTGGGGTGGCTTAGGGCCCAAGCCCCCGGCTCCAAAAGCTCCCAAGGGCGCTCCC	351						
Qy	225	CAGGCAACGGTGCTCGGGCCCTTCCTTCGGTCAGAAAAGTCGGCCCTGGGGGCGAGTTGCTC	284						
Db	352	CAGGCAACGGTGCTCGGGCCCTTCCTTCGGTCAGAAAAGTCGGCCCTGGGGGCGAGTTGCTC	411						
Qy	285	CCAAAGGGTTTCCTCGAAAAGAACTCTGAGAGGGCGGAGTCTTGACGAGGGAAATCTCTCT	344						
Db	412	CCAAAGGGTTTCCTCGAAAAGAACTCTGAGAGGGCGGAGTCTTGACGAGGGAAATCTCTCT	471						
Qy	345	GTGTAGCTTGGAAAGCGCCAGCCCCCAGAAAGATGGCTGCCTTCAATAGATTGTTTCCCGCT	404						
Db	472	GTGTAGCTTGGAAAGCGCCAGCCCCCAGAAAGATGGCTGCCTTCAATAGATTGTTTCCCGCT	531						
Qy	405	GGCTTCTCTCGTGCTTATCTACTACGGG	430						
Db	532	GGCTTCTCTCGTGCTTATCTACTACGGG	557						

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RESULT 12
US-09-925-065A-774904
; Sequence 774904, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
;   Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 774904
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-774904

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323 |||||||
Db    264 GACTCTGGCCTTCTACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGCGGCATCGGCC
Qy    775 TTTGTGAAGACGACGCGGCTGATCCCCCTAAAGAGTCAC 812
Db    324 TTTGTGAAGACGACGCGGCTGATCCCCCTAAAGAGTCAC 361

RESULT 13
US-10-450-763-22566
; Sequence 22566, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CI P3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22566
; LENGTH: 621
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (40)..(282)
; OTHER INFORMATION: 95% homologous to Rattus norvegicus voltage-gated sodium channel beta-3 subunit, accession number AJ243395, Smith-US-10-450-763-22566
; OTHER INFORMATION: Score=397.
US-10-450-763-22566

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RESULT 14
US-09-764-891-7659
; Sequence 7659, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 7659

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; LENGTH: 4625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-891-7659

Query Match      17.1%; Score 216; DB 3; Length 4625;
Best Local Similarity 100.0%; Pred.No. 7.3e-107;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1044 AGGTGGCCTGAACACCTGAGGACTGGACATCCCATGTTTCAGCAATGTCATATGGCATCAG 1103
DB 33 AGGTGGCCTGAACACCTGAGGACTGGACATCCCATGTTTCAGCAATGTCATATGGCATCAG 92
QY 1104 GAGGCGGCCCAAGGGCCCCATCGCTTCCCTTCATGATCCATTGTTCTGTTCAATTCATT 1163
DB 93 GAGGCGGCCCAAGGGCCCCATCGCTTCCCTTCATGATCCATTGTTCTGTTCAATTCATT 152
QY 1164 CATCATATACATCCACCTGCTCTGAGCTTTTCACTCTGACTCCCTAACTCCATCAGACCT 1223
DB 153 CATCATATACATCCACCTGCTCTGAGCTTTTCACTCTGACTCCCTAACTCCATCAGACCT 212
QY 1224 CTAGCACCATAAGACTCTGCCAGAACTGAGAAGCC 1259
DB 213 CTAGCACCATAAGACTCTGCCAGAACTGAGAAGCC 248
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RESULT 15
US-10-276-774-718/c
; Sequence 718, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 718
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-718
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Query Match      7.2%; Score 91; DB 7; Length 407;
Best Local Similarity 99.3%; Pred.No. 1.6e-38;
Matches 141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 820 GCTGGAGAGGACTTCACCTCTGTGGTCTCAGAAATCATGATGATCATCTTCTGTCTTC 879
DB 230 GCTGGAGAGGACTTCACCTCTGTGGTCTCAGAAATCATGATGATCATCTTCTGTCTTC 171
QY 880 CTCACCTGTGGTCTGCTCATCGAGATGATATATTCCTACAGAAAGGTCTCAAAAGCCGAA 939
DB 170 CTCACCTGTGGTCTGCTCATCGAGATGATATATTCCTACAGAAAGGTCTCAAAAGCCGAA 111
QY 940 GAGGCGGCCCAAGGGCCCCATCGCTTCCCTTCATGATCCATTGTTCTGTTCAATTCATT 961
DB 110 GAGGCGGCCCAAGGGCCCCATCGCTTCCCTTCATGATCCATTGTTCTGTTCAATTCATT 89
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Search completed: December 13, 2005, 17:17:59
Job time : 1164 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 14:43:17 ; Search time 213 Seconds
(without alignments)

2213.290 Million cell updates/sec

Title: US-09-977-579A-4

Perfect score: 1261

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Gapop 60.0, Gapext 60.0

Searched: 3392430 seqs, 186927314 residues

Word size: 10

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Post-processing: Listing first 45 summaries

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- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
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- 8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1261	100.0	1261	6	US-10-374-954-8
2	50	4.0	880	6	US-10-750-185-44336
3	19	1.5	19	8	US-11-101-244-1098655
4	19	1.5	19	8	US-11-101-244-1098661
5	19	1.5	19	8	US-11-101-244-1098665
6	19	1.5	19	8	US-11-101-244-1098671
7	19	1.5	19	8	US-11-101-244-1098679
8	19	1.5	19	8	US-11-101-244-1098688
9	19	1.5	19	8	US-11-101-244-1098692
10	19	1.5	19	8	US-11-101-244-1098695
11	19	1.5	19	8	US-11-101-244-1098711
12	19	1.5	19	8	US-11-101-244-1098717
13	19	1.5	19	8	US-11-101-244-1098723
14	19	1.5	19	8	US-11-101-244-1098724
15	19	1.5	19	8	US-11-101-244-1098725
16	19	1.5	19	8	US-11-101-244-1098733
17	19	1.5	19	8	US-11-101-244-1098734
18	19	1.5	19	8	US-11-101-244-1098740
19	19	1.5	19	8	US-11-101-244-1098746
20	19	1.5	19	8	US-11-101-244-1098748
21	19	1.5	19	8	US-11-101-244-1098755
22	19	1.5	19	9	US-11-083-784-1098661
23	19	1.5	19	9	US-11-083-784-1098665

24	19	1.5	19	9	US-11-083-784-1098671	Sequence 1098671,
25	19	1.5	19	9	US-11-083-784-1098679	Sequence 1098679,
26	19	1.5	19	9	US-11-083-784-1098688	Sequence 1098688,
27	19	1.5	19	9	US-11-083-784-1098692	Sequence 1098692,
28	19	1.5	19	9	US-11-083-784-1098695	Sequence 1098695,
29	19	1.5	19	9	US-11-083-784-1098711	Sequence 1098711,
30	19	1.5	19	9	US-11-083-784-1098717	Sequence 1098717,
31	19	1.5	19	9	US-11-083-784-1098723	Sequence 1098723,
32	19	1.5	19	9	US-11-083-784-1098724	Sequence 1098724,
33	19	1.5	19	9	US-11-083-784-1098725	Sequence 1098725,
34	19	1.5	19	9	US-11-083-784-1098733	Sequence 1098733,
35	19	1.5	19	9	US-11-083-784-1098734	Sequence 1098734,
36	19	1.5	19	9	US-11-083-784-1098740	Sequence 1098740,
37	19	1.5	19	9	US-11-083-784-1098746	Sequence 1098746,
38	19	1.5	19	9	US-11-083-784-1098748	Sequence 1098748,
C 39	19	1.5	1360	6	US-10-750-185-51249	Sequence 51249, A
40	19	1.5	1573	6	US-10-750-185-28594	Sequence 28594, A
41	19	1.5	114801	7	US-11-121-086-22	Sequence 22, Appl
42	18	1.4	755	6	US-10-750-185-43762	Sequence 43762, A
C 43	18	1.4	1292	6	US-10-750-185-24891	Sequence 24891, A
C 44	18	1.4	1480	7	US-11-112-908-437	Sequence 437, App
C 45	18	1.4	1887	6	US-10-750-185-25968	Sequence 25968, A

ALIGNMENTS

RESULT 1
US-10-374-954-8
; Sequence 8, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (376)..(1023)
US-10-374-954-8

Query Match	100.0%;	Score 1261;	DB 6;	Length 1261;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1261;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CCCTCCCTCCGAGCTGAGCTTACCTCGGGCGGCAACGAGCGAGGCGGCGGCGAGTGG	60	
Db	1	CCCTCCCTCCGAGCTGAGCTTACCTCGGGCGGCAACGAGCGAGGCGGCGGCGAGTGG	60	
Qy	61	AAGCTGAGTTCGCGGGTGGCGGGAGGCGGAGTGTCCGTGCTGCTGAGCGCCGCGGAGA	120	
Db	61	AAGCTGAGTTCGCGGGTGGCGGGAGGCGGAGTGTCCGTGCTGCTGAGCGCCGCGGAGA	120	
Qy	121	CGCGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCTAGTGGGTCGCTTAG	180	
Db	121	CGCGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCTAGTGGGTCGCTTAG	180	
Qy	181	GGCCCAAGCCCCCACCACCGGCTCCAAAGTCTCCAGGGCTCCCCAGGACCGGTCTCG	240	
Db	181	GGCCCAAGCCCCCACCACCGGCTCCAAAGTCTCCAGGGCTCCCCAGGACCGGTCTCG	240	

Qy 241 GCCCTTCCTTCGGTCAGAAAGTCGCCCTCGGGGCGAGTTGTCCTCCAAAGGGTTTCCTCG 300
Db 241 GCCCTTCCTTCGGTCAGAAAGTCGCCCTCGGGGCGAGTTGTCCTCCAAAGGGTTTCCTCG 300
Qy 301 AAAGAACTGAGAGGGGCGAGTCCTTGACCCAGGGAATCTCTGTGTAGGCTTGGAGC 360
Db 301 AAAGAACTGAGAGGGGCGAGTCCTTGACCCAGGGAATCTCTGTGTAGGCTTGGAGC 360
Qy 361 CGCCAGGCCCCAGAGATGSCCTGCTCAATAGATTGTTTCCCTCGGCTTCTCTCGTCTT 420
Db 361 CGCCAGGCCCCAGAGATGSCCTGCTCAATAGATTGTTTCCCTCGGCTTCTCTCGTCTT 420
Qy 421 ATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGCGAGGCC 480
Db 421 ATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGCGAGGCC 480
Qy 481 GTGAGGGCAACCCGATGAAGTCGGTGCATCTCTGTCATGAAGAGAGAGGAGTGGAG 540
Db 481 GTGAGGGCAACCCGATGAAGTCGGTGCATCTCTGTCATGAAGAGAGAGGAGTGGAG 540
Qy 541 GCCACCGGTGGTGAATGTTCTACAGGCCCGAGGCGGTAAAGATTTCTTATTAT 600
Db 541 GCCACCGGTGGTGAATGTTCTACAGGCCCGAGGCGGTAAAGATTTCTTATTAT 600
Qy 601 GAGTATCGGAATGGCCACGAGGAGTGGAGAGCCCTTTTCAGGGGCGCTGCACTGGAAT 660
Db 601 GAGTATCGGAATGGCCACGAGGAGTGGAGAGCCCTTTTCAGGGGCGCTGCACTGGAAT 660
Qy 661 GGCAGAAAGACCTGACGAGAGTGTTCATCTGTGTCTCAACGTCATCTGAAACGACTCT 720
Db 661 GGCAGAAAGACCTGACGAGAGTGTTCATCTGTGTCTCAACGTCATCTGAAACGACTCT 720
Qy 721 GGCCTCTACCTGCAATGTCCTCGGAGTTTTCAGTTTGAAGGCGCATCGGCCCTTTGTG 780
Db 721 GGCCTCTACCTGCAATGTCCTCGGAGTTTTCAGTTTGAAGGCGCATCGGCCCTTTGTG 780
Qy 781 AAGACGACGCGGCTGATCCCCCTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACCTCT 840
Db 781 AAGACGACGCGGCTGATCCCCCTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACCTCT 840
Qy 841 GTGGTCTCAGAAATCATGATGATACATCTTCTGTGCTTTCCTCACCTGTGCTGCTCATC 900
Db 841 GTGGTCTCAGAAATCATGATGATACATCTTCTGTGCTTTCCTCACCTGTGCTGCTCATC 900
Qy 901 GAGATGATATATTGCTACAGAAAGTCTCAAAAGCGAAGAGGAGGAGCCCAAGAAACGCG 960
Db 901 GAGATGATATATTGCTACAGAAAGTCTCAAAAGCGAAGAGGAGGAGCCCAAGAAACGCG 960
Qy 961 TCTGACTACCTTGCCATCCCATCTGAGAAACAGGAGAACTCTGGGTTACCAAGTGGAGAA 1020
Db 961 TCTGACTACCTTGCCATCCCATCTGAGAAACAGGAGAACTCTGGGTTACCAAGTGGAGAA 1020
Qy 1021 TAGAACAGGACAGTGTGACATGAGTGGCTGTGAACACCTGAGGAGCTGGACATCCCATG 1080
Db 1021 TAGAACAGGACAGTGTGACATGAGTGGCTGTGAACACCTGAGGAGCTGGACATCCCATG 1080
Qy 1081 TTCAGCATCTCAATGGCATCAGAGGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGC 1140
Db 1081 TTCAGCATCTCAATGGCATCAGAGGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGC 1140
Qy 1141 ATCCATTTGTTGTTTCATTTTCATCATCATCATCATCATCATCATCATCATCATCATCT 1200
Db 1141 ATCCATTTGTTGTTTCATTTTCATCATCATCATCATCATCATCATCATCATCATCATCT 1200
Qy 1201 GACTCCCTTAATCCATCAGACTCTPACGCAACATAAGACTCTGCGAGAACTTGAGAAGCG 1260
Db 1201 GACTCCCTTAATCCATCAGACTCTPACGCAACATAAGACTCTGCGAGAACTTGAGAAGCG 1260
Qy 1261 G 1261
Db 1261 G 1261

RESULT 2
US-10-750-185-44336
; Sequence 44336, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44336
; LENGTH: 880
; TYPE: DNA
; ORGANISM: Bovine 19866808098198
US-10-750-185-44336
Query Match 4.0%; Score 50; DB 6; Length 880;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 820 GCTGGAGGAGGACTTCACCTCTGTGGTCTCAGAAATCATGATGATCATCTCT 869
Db 443 GCTGGAGGAGGACTTCACCTCTGTGGTCTCAGAAATCATGATGATCATCTCT 492
RESULT 3
US-11-101-244-1098655
; Sequence 1098655, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098655
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098655
Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.9;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Qy 903 GATGATATATGCTTACAGA 921
Db 1 GAUGAUUAUUGCUACAGA 19
RESULT 4
US-11-101-244-1098661

; Sequence 1098661, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098661
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098661

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.9;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 331 GAGGAATCTCTGTGTGTA 349
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Db 1 GAGGAAAUUCUCUGUGUA 19

RESULT 5
US-11-101-244-1098665
; Sequence 1098665, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098665
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098665

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.9;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 711 GAACGACTCTGGCTCTAC 729
|||||:|:|:|:|:|:|:
Db 1 GAACGACUCUGGCCUCUAC 19

RESULT 6
US-11-101-244-1098671
; Sequence 1098671, Application US/11101244

; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098671
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098671

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.9;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 845 TCTCAGAAATCATGATGTA 863
|||||:|:|:|:|:|:|:
Db 1 UCUCAGAAAUCAUGUGUA 19

RESULT 7
US-11-101-244-1098679
; Sequence 1098679, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098679
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098679

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 57.9%; Pred. No. 2.9;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
QY 579 CGGTAAGATTTCTTTATT 597
|||||:|:|:|:|:|:|:
Db 1 CGGAAAGAUUCCUUAU 19

RESULT 8
US-11-101-244-1098688
; Sequence 1098688, Application US/11101244
; Publication No. US20050246794A1

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; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIORITY FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098688
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098688
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Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 57.9%; Pred. No. 2.9;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
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Qy 1153 GTTCATTCATTCATCCATA 1171
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Db 1 GUCAUUAUUAUUAUUAUUA 19
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RESULT 9

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US-11-101-244-1098692
; Sequence 1098692, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIORITY FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098692
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098692
```

```
Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 937 GAAGAGGAGCCCAAGAAA 955
|:|:|:|:|:|:|:|:|:|:|
Db 1 GAAGAGGAGCCCAAGAAA 19
```

RESULT 10

```
US-11-101-244-1098695
; Sequence 1098695, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIORITY FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098695
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098695
```

```
Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.9;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 901 GAGATGATATATTCCTACA 919
|:|:|:|:|:|:|:|:|:|:|
Db 1 GAGAUAUAUAUUAUUAUUA 19
```

RESULT 11

```
US-11-101-244-1098711
; Sequence 1098711, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIORITY FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098711
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098711
```

```
Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.9;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 763 GCGCATCGGCCCTTTGTGA 781
|:|:|:|:|:|:|:|:|:|:|
Db 1 GCGCAUCGCGCCCUUGUGA 19
```

RESULT 12

```
US-11-101-244-1098717
; Sequence 1098717, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
```


; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098717
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098717

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 936 CGAAGAGGCGCCCAAGAA 954
|||||
Db 1 CGAAGAGGCGCCCAAGAA 19

RESULT 13
US-11-101-244-1098723
; Sequence 1098723, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098723
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098723

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.9;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1038 GACATGAGTGGCCTGAAC 1056
|||||
Db 1 GACAUGAGGUGCCUGAAC 19

RESULT 14
US-11-101-244-1098724
; Sequence 1098724, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098724
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098724

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1023 GAACAGAGCAGTGTGACA 1041
|||||
Db 1 GAACAGAGCAGUGUGACA 19

RESULT 15
US-11-101-244-1098725
; Sequence 1098725, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098725
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098725

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.9;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 993 GGAGAACTCTGCGGTACCA 1011
|||||
Db 1 GGAGAACUCUGCGGUACCA 19

Search completed: December 13, 2005, 17:21:37
Job time : 214 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 13, 2005, 14:47:42 ; Search time 193 Seconds
(without alignments)
1980.185 Million cell updates/sec

Title: US-09-977-579A-2

Perfect score: 1124

Sequence: 1 MPANRLFLPLASLVLYWVS.....SDYLAIPSENKENSAPVVEE 215

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=issued_Patents_NA -QFm=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0

-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bloms62 -TRANS=human40.cdi

-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15

-MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-USR=US09977579 @CGN 1.1 193 @runat_09122005_123005_26865 -NCPU=6 -ICPU=3

-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG

-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents_NA:

1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*

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5: /cgn2_6/ptodata/1/ina/H COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*

9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470	41.8	617	3	US-09-949-016-2369 Sequence 2369, Ap
2	165.5	14.7	11174	3	US-09-949-016-14111 Sequence 14111, A
3	165.5	14.7	30337	3	US-09-949-016-13053 Sequence 13053, A
4	147	13.1	1342	3	US-09-949-016-787 Sequence 787, App
5	147	13.1	1371	3	US-09-991-181-388 Sequence 388, App
6	147	13.1	1371	3	US-09-991-181-388 Sequence 388, App
7	147	13.1	1371	3	US-09-997-333-388 Sequence 388, App
8	147	13.1	1371	3	US-09-992-598-388 Sequence 388, App
9	147	13.1	1708	3	US-09-949-016-4948 Sequence 4948, Ap

10	131	11.7	1121	3	US-09-949-016-5103 Sequence 5103, Ap
11	131	11.7	1151	3	US-09-430-503-1 Sequence 1, Appli
12	131	11.7	1151	3	US-09-430-503-3 Sequence 3, Appli
13	131	11.7	1151	3	US-09-430-503-5 Sequence 5, Appli
14	131	11.7	1151	3	US-09-430-503-7 Sequence 7, Appli
15	131	11.7	1151	3	US-10-095-131A-1 Sequence 1, Appli
16	131	11.7	1151	3	US-10-095-131A-3 Sequence 3, Appli
17	131	11.7	1151	3	US-10-095-131A-5 Sequence 5, Appli
18	131	11.7	1151	3	US-10-095-131A-7 Sequence 7, Appli
19	131	11.7	1777	3	US-10-012-231A-363 Sequence 363, App
20	131	11.7	1777	3	US-10-015-389A-363 Sequence 363, App
21	131	11.7	1777	3	US-10-006-768A-363 Sequence 363, App
22	131	11.7	1777	3	US-10-015-671A-363 Sequence 363, App
23	131	11.7	1777	3	US-10-015-393A-363 Sequence 363, App
24	131	11.7	1777	3	US-10-011-833A-363 Sequence 363, App
25	131	11.7	1777	3	US-10-006-041A-363 Sequence 363, App
26	131	11.7	1777	3	US-10-012-064A-363 Sequence 363, App
27	129	11.5	600	3	US-09-430-503-43 Sequence 43, Appl
28	129	11.5	600	3	US-09-430-503-47 Sequence 47, Appl
29	129	11.5	600	3	US-10-095-131A-43 Sequence 43, Appl
30	129	11.5	600	3	US-10-095-131A-47 Sequence 47, Appl
31	127	11.3	600	3	US-09-430-503-41 Sequence 41, Appl
32	127	11.3	600	3	US-09-430-503-45 Sequence 45, Appl
33	127	11.3	600	3	US-10-095-131A-41 Sequence 41, Appl
34	127	11.3	600	3	US-10-095-131A-45 Sequence 45, Appl
35	127	11.3	752	3	US-09-430-503-17 Sequence 17, Appl
36	127	11.3	752	3	US-09-430-503-19 Sequence 19, Appl
37	127	11.3	752	3	US-09-430-503-21 Sequence 21, Appl
38	127	11.3	752	3	US-09-430-503-23 Sequence 23, Appl
39	127	11.3	752	3	US-10-095-131A-17 Sequence 17, Appl
40	127	11.3	752	3	US-10-095-131A-19 Sequence 19, Appl
41	127	11.3	752	3	US-10-095-131A-21 Sequence 21, Appl
42	127	11.3	752	3	US-10-095-131A-23 Sequence 23, Appl
43	125	11.1	1073	3	US-09-430-503-25 Sequence 25, Appl
44	125	11.1	1073	3	US-09-430-503-27 Sequence 27, Appl
45	125	11.1	1073	3	US-09-430-503-29 Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-2369
; Sequence 2369, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2369
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2369

Alignment Scores:
Pred. No.: 2.91e-50 Length: 617
Score: 470.00 Matches: 101
Percent Similarity: 66.16% Conservative: 30
Best Local Similarity: 51.01% Mismatches: 59
Query Match: 41.81% Indels: 8
DB: 3 Gaps: 5

, APPLICANT: Gurney, Austin L.
, APPLICANT: Kljavin, Ivar J.
, APPLICANT: Napier, Mary A.
, APPLICANT: Pan, James
, APPLICANT: Paoni, Nicholas F.
, APPLICANT: ROY, Margaret Ann
, APPLICANT: Stewart, Timothy A.
, APPLICANT: Tunas, Daniel
, APPLICANT: Watanabe, Colin K.
, APPLICANT: Williams, P. Mickey
, APPLICANT: Wood, William I.
, APPLICANT: Zhang, Zemin
, TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
, FILE REFERENCE: P2730P1C3
, CURRENT APPLICATION NUMBER: US/09/991,181
, CURRENT FILING DATE: 2001-11-16
, PRIOR APPLICATION NUMBER: 60/049787
, PRIOR FILING DATE: 1997-06-16
, PRIOR APPLICATION NUMBER: 60/062250
, PRIOR FILING DATE: 1997-10-17
, PRIOR APPLICATION NUMBER: 60/065186
, PRIOR FILING DATE: 1997-11-12
, PRIOR APPLICATION NUMBER: 60/065311
, PRIOR FILING DATE: 1997-11-13
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 ; PRIOR APPLICATION NUMBER: 60/090695
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 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 1,22e-08 Length: 1371
 Score: 147.00 Matches: 57
 Percent Similarity: 41.44% Conservative: 35
 Best Local Similarity: 25.68% Mismatches: 80
 Query Match: 13.08% Indels: 50
 DB: 3 Gaps: 9

US-09-977-579A-2 (1-215) x US-09-991-181-388 (1-1371)

Qy 7 LeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCys 26
 Db 181 CTTTGGCCCTATAGCAGCT--GTGGAATTTATATACCTCCCGGGT----- 222
 Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
 Db 223 -----CTGAGCGCTGTTAATGGACAGATGCTCGGTTAAATGCACT 264
 Qy 47 SerCysMetLysArgGluGluValGluAlaThrThrValValGluTrpPheTyrArgPro 66
 Db 265 TTCTCCAGCTTTGCCCTGTGGTGATGCTCTAACAGTGACC---TGGAATTTTCGTCT 321
 Qy 67 ---GluGlyGly---LysAspPheLeuIleTyrGluTyrArgAsnGlyHisGlnGluVal 84
 Db 322 CTAGACGGGGACCTGACGAGCTTTGTATTCTACCATAGATGCTCCATCCACCCATG 381
 Qy 85 GluSerProGlnGlyArgGlnTrpAsnGlySerLysAspLeuGlnAspValSer 104
 Db 382 AGTGGCGGTTAAGACCGGGTGTCTTGGATGGGAATCTCGACGGTACGATGCTCCTCC 441
 Qy 105 IleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSerArg 124
 Db 442 ATCTTCTCTGMAACTCAGTTTCGACCAATGGACATACACCTGCCAGGTGAAGAAC 501

Qy 125 GluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeuIleProLeuArg 144
 Db 502 -----CCACCTGAT 510
 Qy 145 ValThrGluGluAlaGlyGluAspPheThrSerValVal-----SerGlu 159
 Db 511 GTTGATGGGGTGATAGGGAGATCCGGCTCAGCGTCTGTGCACACTGTACCGCTTCTCTGAG 570
 Qy 160 IleMetMetTyrIleLeuLeuVal-----PheLeuThrLeuTrpLeu 173
 Db 571 ATCCACTTCTGGCTCTGGCCATTTGGCTGTGCCTGTGCCTGATGATCATATAGTAATT 630
 Qy 174 LeuIleGluMetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaGlnGlu 193
 Db 631 GTAGTGGTCTCTTCCAGCATTAACCGGAAAAAGCGATGGCGCGGAAGAGCT----- 681
 Qy 194 AsnAlaSerAspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProVal 213
 Db 682 -----CATAAAGTGGTGAGATAAAATCAAAAGAGAGAAAGGCTCAACCAA 729
 Qy 214 GluGlu 215
 Db 730 GAGAAA 735

RESULT 6

US-09-990-444-388
 ; Sequence 388, Application US/09990444
 ; Patent No. 6930170

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C19
 ; CURRENT APPLICATION NUMBER: US/09/990,444
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066770
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/075945
 ; PRIOR FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 1 22e-08 Length: 1371
Score: 147.00 Matches: 57
Percent Similarity: 41.44% Conservative: 35
Best Local Similarity: 25.68% Mismatches: 80
Query Match: 13.08% Indels: 50
DB: 3 Gaps: 9

US-09-977-579A-2 (1-215) x US-09-990-444-388 (1-1371)

Qy 7 LeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCys 26
Db 181 CTTTGGCCTATAGAGCT--GTGAAATTTATACCTCCCGGTG-----222
Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 223 -----CTGGAGGCTGTTAATGGGACAGATGCTCGGTTTAAATGCACCT 264
Qy 47 SerCysMetLysArgGluValGluAlaThrThrValValGluTyrPheTyrArgPro 66
Db 265 TTCTCCAGCTTTGCCCTGGGGTGATGCTCTACAGTGACC---TGGAAATTTTCGTCT 321
Qy 67 ---GluGlyGly---LysAspPheLeuIleTyrGluTyrArgAsnGlyHisGlnGluVal 84
Db 322 CTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTCCAACCCATG 381
Qy 85 GluSerProGlnGlyArgLeuGlnTyrAsnGlySerLysAspLeuGlnAspValSer 104
Db 382 AGTGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGATGCTCC 441
Qy 105 IleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSerArg 124
Db 442 ATCTTCTCTGGAACTGCGAGTTCGACGACAAATGGGACATACACCTCCAGGTGAAGAAC 501
Qy 125 GluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeuIleProLeuArg 144
Db 502 -----CCACCTGAT 510
Qy 145 ValThrGluGluAlaGlyGluAspPheThrSerValVal-----SerGlu 159
Db 511 GTTGATGGGTGATAGGGAGATCCGGCTCAGCGCTCGTGCACACATGTCGCTTCTCTGAG 570
Qy 160 IleMetMetTyrIleLeuLeuVal-----PheLeuThrLeuTyrLeu 173
Db 571 ATCCACTTCTGGCTCTGGCCATTGGCTCTGCCCTGTCGATGATGATCATAGTAAAT 630
Qy 174 LeuIleGluMetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaAaGlnGlu 193
Db 631 GTAGTGTCTCTCTCCAGCATTACCGGAAAGCGATGGGCCGAAAGAGCT-----681
Qy 194 AsnAlaSerAspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProVal 213
Db 682 -----CATAAAGTGGTGGAGATAAAATCAAAAGAGGAAGGAGGCTCAACCAA 729
Qy 214 GluGlu 215
Db 730 GAGAAA 735

RESULT 7

US-09-977-333-388
; Sequence 388, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tuma, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C27
; CURRENT APPLICATION NUMBER: US/09/997,333
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
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; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167

Qy 67 ---GluGlyGly---LysAspPheLeuIleTyrGluTyrArgAenglyHisGlnGluVal 84
Db 322 CTAGACGGGGAGCTGAGTGTGTTATCTTACACACATAGATCCCTTCCACCCCATG 381
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Db 382 AGTGGGGGTTTAGGACCGGGTCTTGGATGGGAATCCTGACCGGTAGATGCCCTCC 441
Qy 105 IleThrValLeuAenValThrLeuAsnAspSerGlyLeuTyrThrCysAenValSerArg 124
Db 442 ATCTCTCTCGAAATGTCAGTTCGACACAATGGACATACACCTGCCAGGTGAAGAAC 501
Qy 125 GluPheGluPheGluAlaHisArgProPheVallysthrThrArgLeuIleProLeuArg 144
Db 502 -----CCACCTGAT 510
Qy 145 ValThrGluGluAlaGlyGluAspPheThrSerValVal-----SerGlu 159
Db 511 GTTGATGGGTGATAGGGAGATCCGGCTCAGCGTCGTGCACATGATACGTTCTCTGAG 570
Qy 160 IleMetMetTyrIleLeuLeuVal-----PheLeuThrLeuTrpLeu 173
Db 571 ATCCACTCTCGGCTCTGCCCATGGCTCTGCCCTGTGCACGTGATCATATAAGTAATT 630
Qy 174 LeuIleGluMetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaGlnGlu 193
Db 631 GTAGTGGTCTCTCTCCAGCATTTACCGGAAAGCGATGGCGCGAAGAGCT----- 681
Qy 194 AsnAlaSerAspTyrLeuAlaIleProSerGluAenLysGluAenSerAlaValProVal 213
Db 682 -----CATRAAGTGGTGAGATATAATCAAAAGAAAGAGGAAAGGCTCAACCAA 729
Qy 214 GluGlu 215
Db 730 GAGAAA 735

RESULT 8

US-09-992-598-388
; Sequence 388, Application US/09992598

; Patent No. 6956108

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

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; APPLICANT: Gurney, Austin L.

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; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C20

; CURRENT APPLICATION NUMBER: US/09/992,598

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
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; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-05
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
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; PRIOR APPLICATION NUMBER: 60/088826
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; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16

; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
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; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
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; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
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; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 1,22e-08 Length: 1371
Score: 147.00 Matches: 57
Percent Similarity: 41.44% Conservative: 35
Best Local Similarity: 25.68% Mismatches: 80
Query Match: 13.08% Indels: 50
DB: 3 Gaps: 9

US-09-977-579A-2 (1-215) x US-09-992-598-388 (1-1371)

Qy 7 LeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCys 26
Db 181 CTTTGGCCTATAGCAGCT--GTGGAATTTATACCTCCCGGGTG----- 222

Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 223 -----CTGGAGGCTGTTAATGGGACAGATGCTCGTTAAAAATGCAC 264

Qy 47 SerCysMetLysArgGluGluValGluAlaThrThrValValGluTyrPheTyrArgPro 66
Db 265 TTCTCCAGCTTTGCCCTGTGGGTGATGCTCTACAGTGACC---TGAATTTTCGTCT 321

Qy 67 ---GluGlyGly---LysAspPheLeuIleTyrGluTyrArgAsnGlyHisGlnGluVal 84
Db 322 CTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTCCAACCCATG 381

Qy 85 GluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeuGlnAspValSer 104
Db 382 AGTGGGGGTTTAAGGACCGGGTGCTCTGGGATGGGAATCCTGAGCGGTACGATGCCTCC 441

Qy 105 IleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSerArg 124
Db 442 ATCCTTCTCTGGAAACTGCAGTTTCGACGACATATGGGACATACACTGCCAGTGAAGAAC 501

Qy 125 GluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeuIlePheLeuArg 144
Db 502 -----CCACCTGAT 510

Qy 145 ValThrGluGluAlaGlyGluAspPheThrSerValVal-----SerGlu 159
Db 511 GTTGATGGGTGATAGGGGAGATCCGGCTCAGCGCTCGTGACACTGTACGTCTTCTGAG 570

Qy 160 IleMetMetTyrIleLeuLeuVal-----PheLeuThrLeuTrpLeu 173
Db 571 ATCCACTTCTGGGCTCTGGCCATTGGCTCTCCCTGTGCACCTGATGATCATATAGTAATT 630

Qy 174 LeuIleGluMetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaAalaGlnGlu 193
Db 631 GTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCATGGGCGGAAAGAGCT----- 681

Qy 194 AsnAlaSerAspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProVal 213
Db 682 -----CATAAAGTGTGGAGATAAAATCAAAAGAAAGAGAAAGGCTCAACCAA 729


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Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu--- 159
Db 550 ---CCTCTGACATCGTTGTCCAGCTGGACACATAGGCTCTATGCTGTAGAGAAAAGAG 606
Qy 160 -----IleMetMetTyrIleLeuLeuValPheLeuThr 170
Db 607 AATTGGCTGGTTTCCAGTTTGGGTAGTGGGCGATAGTTACTGTGCTGTCTTAGGT 666
Qy 171 LeuTrpLeuLeuIleGluMetIleTyrCys-----TyrArgLys----- 183
Db 667 CTCACCTCTGCTCATCAGCATGATTCGTGCTCTCTATAGAGGAAAACCTCTAAACGG 726
Qy 184 -----ValSerLysAlaGluGluAlaAalaglnGlu 193
Db 727 GATTACACTGCTGCAGTACATCAGAGAGTTTGTCCAGTTAAGCAGGCTCTCGGAAG 786
Qy 194 AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer 209
Db 787 TCCCCCTCCGACACTGAGGGCTTGTAAAGAGTCTGCCTTCTGGATCTCCACGAGGCCA 846
Qy 210 AlaVal 211
Db 847 GTCATA 852

RESULT 11
US-09-430-503-1
; Sequence 1, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (P2R) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Gene
; LOCATION: (1)..(1151)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (133)..(939)
US-09-430-503-1

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Pred. No.: 1.02e-06 Length: 1151
Score: 131.00 Matches: 51
Percent Similarity: 37.39% Conservative: 32
Best Local Similarity: 22.97% Mismatches: 81
Query Match: 11.65% Indels: 58
DB: 3 Gaps: 9

US-09-977-579A-2 (1-215) x US-09-430-503-1 (1-1151)
Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 250 GTATATACGCCAAAGAAATCTCTGTCGAATGTTACACAGGGGAAGCTGACCTGC--- 306
Qy 47 SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe 63
Db 307 -----AAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTCTCTCGGAGC 357
Qy 64 TyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln 82
Db 358 TTCCAGCCAGAGGGGGCCGACACTACTGTGTGCTGTTTTTCCACTACTCCCAAGGGCAAGTG 417
Qy 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
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Db 418 TACCTTGGGAATTATCACCATTAAAGACAGAATCAGCTGGCTGGAGACCTTGACAAG 477
Qy 101 GluAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuThrCys 120
Db 478 AAGATGATCATCAATCAACATAGAAAATATACGATTTTATACACAATGGCACCCTATATCTGT 537
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 538 GATGTCAAAAC----- 549
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu--- 159
Db 550 ---CCTCTGACATCGTTGTCCAGCTGGACACATAGGCTCTATGCTGTAGAGAAAAGAG 606
Qy 160 -----IleMetMetTyrIleLeuLeuValPheLeuThr 170
Db 607 AATTGGCTGTGTTCCAGTTTGGGTAGTGGGCGATAGTTACTGTGCTGTCTTAGGT 666
Qy 171 LeuTrpLeuLeuIleGluMetIleTyrCys-----TyrArgLys----- 183
Db 667 CTCACCTCTGCTCATCAGCATGATTCGTGCTCTCTATAGAGGAAAACCTCTAAACGG 726
Qy 184 -----ValSerLysAlaGluGluAlaAalaglnGlu 193
Db 727 GATTACACTGCTGCAGTACATCAGAGAGTTTGTCCAGTTAAGCAGGCTCTCGGAAG 786
Qy 194 AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer 209
Db 787 TCCCCCTCCGACACTGAGGGCTTGTAAAGAGTCTGCCTTCTGGATCTCCACGAGGCCA 846
Qy 210 AlaVal 211
Db 847 GTCATA 852

RESULT 12
US-09-430-503-3
; Sequence 3, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (P2R) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Gene
; LOCATION: (1)..(1151)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (133)..(939)
US-09-430-503-3

Alignment Scores:
Pred. No.: 1.02e-06 Length: 1151
Score: 131.00 Matches: 51
Percent Similarity: 37.39% Conservative: 32
Best Local Similarity: 22.97% Mismatches: 81
Query Match: 11.65% Indels: 58
DB: 3 Gaps: 9

US-09-977-579A-2 (1-215) x US-09-430-503-3 (1-1151)
Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 250 GTATATACGCCAAAGAAATCTCTGTCGAATGTTACACAGGGGAAGCTGACCTGC--- 306
```

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Qy 47 SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe 63
Db 307 -----AAGTTCAAGTCTACTAGTACGACTGGCGGTTGACCTCGTCTCTCGGAGC 357
Qy 64 TyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln 82
Db 358 TTCGAGCAGAGGGGGCGACACTACTGTGTGTCGTTTTCACACTACTCCCAAGGCAAGTG 417
Qy 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 418 TACCTTGGGAATTATCCACATTTAAAGACAGAAATCAGCTGGCTGGAGACCTTGACAAG 477
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 478 AAAGATGCATCAATCAACATAGAAAATATGAGTTTATACAAATGGCACCTATATCTGT 537
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 538 GATGTCAAAAC----- 549
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValSerGlu--- 159
Db 550 ---CCTCTGCATCGTTGTCAGCCTGGACACATTAGGCTCTATGTCGTAGAAAAGAG 606
Qy 160 -----IleMetMetTyrIleLeuLeuValPheLeuThr 170
Db 607 AATTGCTGTGTTCCAGTTTGGTAGTGGTGGCATAGTTACTGCTGTGCTTAGGT 666
Qy 171 LeuTrpLeuLeuIleGluMetIleTyrCys-----TyrArgLys----- 183
Db 667 CTCACCTGCTCATCAGCATGATTCTGCTGCTCTATAGAGGAACTCTAAACGG 726
Qy 184 -----ValSerLysAlaGluGluAlaAalaGlnGlu 193
Db 727 GATTACACTGGCTGAGTACATCAGAGAGTTTGTACAGTTAAGCAGGCTCTCGGAAG 786
Qy 194 AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer 209
Db 787 TCCCCCTCCGACACTGAGGGCTTTGTAAGAGTCTGCTTCTGATCTCACCAGGGCCCA 846
Qy 210 AlaVal 211
Db 847 GTCATA 852

RESULT 13
US-09-430-503-5
; Sequence 5, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (P2R) AND
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME
; CURRENT APPLICATION NUMBER: US/09/430,503
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1151)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (133)..(939)
US-09-430-503-5

Alignment Scores:
Pred. No.: 1.02e-06 Length: 1151
Score: 131.00 Matches: 51
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Percent Similarity: 37.39% Conservative: 32
Best Local Similarity: 22.97% Mismatches: 81
Query Match: 11.65% Indels: 58
DB: 3 Gaps: 9

US-09-977-579A-2 (1-215) x US-09-430-503-5 (1-1151)
Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 250 GTATATACGCCAAAGAAAATCTTCGTGGCAAAATGGTACACAAAGGAAAGCTGACCTGC--- 306
Qy 47 SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe 63
Db 307 -----AAGTTCAAGTCTACTAGTACGACTGGCGGTTGACCTCGTCTCTCGGAGC 357
Qy 64 TyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln 82
Db 358 TTCGAGCAGAGGGGGCGACACTACTGTGTGTCGTTTTCACACTACTCCCAAGGCAAGTG 417
Qy 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 418 TACCTTGGGAATTATCCACATTTAAAGACAGAAATCAGCTGGCTGGAGACCTTGACAAG 477
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 478 AAAGATGCATCAATCAACATAGAAAATATGAGTTTATACAAATGGCACCTATATCTGT 537
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 538 GATGTCAAAAC----- 549
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValSerGlu--- 159
Db 550 ---CCTCTGCATCGTTGTCAGCCTGGACACATTAGGCTCTATGTCGTAGAAAAGAG 606
Qy 160 -----IleMetMetTyrIleLeuLeuValPheLeuThr 170
Db 607 AATTGCTGTGTTCCAGTTTGGTAGTGGTGGCATAGTTACTGCTGTGCTTAGGT 666
Qy 171 LeuTrpLeuLeuIleGluMetIleTyrCys-----TyrArgLys----- 183
Db 667 CTCACCTGCTCATCAGCATGATTCTGCTGCTCTATAGAGGAACTCTAAACGG 726
Qy 184 -----ValSerLysAlaGluGluAlaAalaGlnGlu 193
Db 727 GATTACACTGGCTGAGTACATCAGAGAGTTTGTACAGTTAAGCAGGCTCTCGGAAG 786
Qy 194 AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer 209
Db 787 TCCCCCTCCGACACTGAGGGCTTTGTAAGAGTCTGCTTCTGATCTCACCAGGGCCCA 846
Qy 210 AlaVal 211
Db 847 GTCATA 852

RESULT 14
US-09-430-503-7
; Sequence 7, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (P2R) AND
; FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME
; CURRENT APPLICATION NUMBER: US/09/430,503
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: Gene
; LOCATION: (1)..(1151)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (133)..(939)
US-09-430-503-7

Alignment Scores:

Pred. No.:	1.02e-06	Length:	1151
Score:	131.00	Matches:	51
Percent Similarity:	37.39%	Conservative:	32
Best Local Similarity:	22.97%	Mismatches:	81
Query Match:	11.65%	Indels:	58
DB:	3	Gaps:	9

US-09-977-579A-2 (1-215) x US-09-430-503-7 (1-1151)

Qy	27	ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle	46
Db	250	GTATATACGCCCAAGAAATCTTCGTGGCAATGGTACACAAAGGGAAGCTGACCTGC---	306
Qy	47	SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe	63
Db	307	-----AAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTCTCCTGGAGC	357
Qy	64	TyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln	82
Db	358	TTCCAGCCAGAGGGCGGCACACTACTGTGCTGCTTTTCCACTACTCCCAAGGCAAGTG	417
Qy	83	GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100
Db	418	TACCTTGGGAATTATCCACCAATTTAAAGACAGAAATCAGCTGGCTGGAGACCTTGACAAG	477
Qy	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120
Db	478	AAAGATGATCAATCAACATAGAAAATATGCAGTTTATACAAATGGCACCCTATATCTGT	537
Qy	121	AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu	140
Db	538	GATGTCAAAAC-----	549
Qy	141	IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu---	159
Db	550	---CCTCCTGACATCGTTGCCAGCTGGACACATAGGCTCTATGTCGTAGAAAAAGAG	606
Qy	160	-----IleMetMetTyrIleLeuLeuValPheLeuThr	170
Db	607	AATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTGCTGTGCTCTAGGT	666
Qy	171	LeuTrpLeuLeuIleGluMetIleTyrCys-----TyrArgLys-----	183
Db	667	CTCACTGTGCTCATCAGCATGATTCTGCTATAGAGGATCTGCTTCTGGATCTCACCAGGGCCCA	726
Qy	184	-----ValSerLysAlaGluGluAlaAlaGlnGlu	193
Db	727	GATTACACTGGCTGCAGTACATCAGAGATTGTGCACAGTTAAGGAAAAAACTCTAAACGG	786
Qy	194	AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer	209
Db	787	TCCCCCTCCGACACTGAGGGTCTTGTAAGAGATCTGCTTCTGGATCTCACCAGGGCCCA	846
Qy	210	AlaVal 211	
Db	847	GTCAATA 852	

RESULT 15

US-10-095-131A-1

; Sequence 1, Application US/10095131A
; Patent No. 6939952
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME

; FILE REFERENCE: Attorney Docket No. 6939952 1242-11/2/2
; CURRENT APPLICATION NUMBER: US/10/095,131A
; CURRENT FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1151)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (133)..(939)
US-10-095-131A-1

Alignment Scores:

Pred. No.:	1.02e-06	Length:	1151
Score:	131.00	Matches:	51
Percent Similarity:	37.39%	Conservative:	32
Best Local Similarity:	22.97%	Mismatches:	81
Query Match:	11.65%	Indels:	58
DB:	3	Gaps:	9

US-09-977-579A-2 (1-215) x US-10-095-131A-1 (1-1151)

Qy	27	ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle	46
Db	250	GTATATACGCCCAAGAAATCTTCGTGGCAATGGTACACAAAGGGAAGCTGACCTGC---	306
Qy	47	SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe	63
Db	307	-----AAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTCTCCTGGAGC	357
Qy	64	TyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln	82
Db	358	TTCCAGCCAGAGGGCGGCACACTACTGTGCTGCTTTTCCACTACTCCCAAGGCAAGTG	417
Qy	83	GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100
Db	418	TACCTTGGGAATTATCCACCAATTTAAAGACAGAAATCAGCTGGCTGGAGACCTTGACAAG	477
Qy	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120
Db	478	AAAGATGATCAATCAACATAGAAAATATGCAGTTTATACAAATGGCACCCTATATCTGT	537
Qy	121	AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu	140
Db	538	GATGTCAAAAC-----	549
Qy	141	IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu---	159
Db	550	---CCTCCTGACATCGTTTCCAGCTGGACACATAGGCTCTATGTCGTAGAAAAAGAG	606
Qy	160	-----IleMetMetTyrIleLeuLeuValPheLeuThr	170
Db	607	AATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTGCTGTGCTCTAGGT	666
Qy	171	LeuTrpLeuLeuIleGluMetIleTyrCys-----TyrArgLys-----	183
Db	667	CTCACTGTGCTCATCAGCATGATTCTGCTATAGAGGATCTGCTTCTGGATCTCACCAGGGCCCA	726
Qy	184	-----ValSerLysAlaGluGluAlaAlaGlnGlu	193
Db	727	GATTACACTGGCTGCAGTACATCAGAGATTGTGCACAGTTAAGGAGGCTCTCGGAAG	786
Qy	194	AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer	209
Db	787	TCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCTTCTGGATCTCACCAGGGCCCA	846
Qy	210	AlaVal 211	

Db 847 GTCATA 852

Search completed: December 13, 2005, 17:25:13
Job time : 210 secs

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US-09-977-579A-2 (1-215) x US-09-977-579-4 (1-1261)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 376 ATGCCTGCCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATCTACTAGGGTCAGT 435

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 436 GTCTGCTTCCCTGTGTGTGAAGTGCCTTCGAGACGGAGGCGGTGCGAGGCAACCCC 495

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 496 ATGAAGCTGCCTGCATCTCTCGATGAAGAGAGAGGAGGTCGAGGCCACCCACCGTGGTG 555

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 556 GAATGGTTCTACAGCCCGAGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 615

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 616 CACGAGGAGGTGGAGAGGCCCTTTTCAGGGGCGCTTCAGTGGATGGCAGCAAGGACTG 675

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 676 CAGGACGTGTCCTCACTGCTCAACGTCACTCTGAACGACTCTGGCTCTACACCTGC 735

Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 736 AATGTGTCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACACGCGGCTG 795

Qy 141 IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 796 ATCCCTTAAGAGTCCAGGAGGCTGGAGGACTTCACCTCTGTGGTCTCAGAAATC 855

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuIleGluMetIleTyrCys 180
Db 856 ATGATGTACATCTTCTGCTTCTCCTACCTGGCTGCTCATCGAGATGATATATGC 915

Qy 181 TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 916 TACAGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACCGGCTCTGACTACCTTGCC 975

RESULT 2

US-10-482-834A-22

; Sequence 22, Application US/10482834A

; Publication No. US20050074764A1

; GENERAL INFORMATION:

; APPLICANT: Harkin, John Charles

; APPLICANT: Harkin, Louise Anne

; APPLICANT: Dibbens, Michelle

; APPLICANT: Wallace, Robyn

; APPLICANT: Phillips, Hilary Ann

; APPLICANT: Heron, Sara Elizabeth

; APPLICANT: Berkovic, Samuel Frank

; APPLICANT: Scheffer, Ingrid Eileen

; APPLICANT: Biomedica Limited

; TITLE OF INVENTION: MUTATIONS IN ION CHANNELS

; FILE REFERENCE: 1386/17

; CURRENT APPLICATION NUMBER: US/10/482,834A

; CURRENT FILING DATE: 2004-01-02

; NUMBER OF SEQ ID NOS: 173

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 22

; LENGTH: 1261

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-482-834A-22

Alignment Scores:

Pred. No.: 3.53e-143 Length: 1261

Score: 1124.00 Matches: 215

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-482-834A-22 (1-1261)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 376 ATGCCTGCCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATCTACTAGGGTCAGT 435

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 436 GTCTGCTTCCCTGTGTGTGAAGTGCCTTCGAGACGGAGGCGGTGCGAGGCAACCCC 495

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 496 ATGAAGCTGCCTGCATCTCTCGATGAAGAGAGAGGAGGTCGAGGCCACCCACCGTGGTG 555

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 556 GAATGGTTCTACAGCCCGAGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 615

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 616 CACGAGGAGGTGGAGAGGCCCTTTTCAGGGGCGCTTCAGTGGATGGCAGCAAGGACTG 675

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 676 CAGGACGTGTCCTCACTGCTCAACGTCACTCTGAACGACTCTGGCTCTACACCTGC 735

Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 736 AATGTGTCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACACGCGGCTG 795

Qy 141 IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 796 ATCCCTTAAGAGTCCAGGAGGCTGGAGGACTTCACCTCTGTGGTCTCAGAAATC 855

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuIleGluMetIleTyrCys 180
Db 856 ATGATGTACATCTTCTGCTTCTCCTACCTGGCTGCTCATCGAGATGATATATGC 915

Qy 181 TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 916 TACAGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACCGGCTCTGACTACCTTGCC 975

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 976 ATCCCATCTGAGAACAGGAGAACTCTGCGGTACCACTGGAGGAA 1020

RESULT 3

US-10-029-191-21

; Sequence 21, Application US/10029191

; Publication No. US20020160453A1

; GENERAL INFORMATION:

; APPLICANT: CURTIS, RORY A.J.

; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT

; FILE OF INVENTION: PROTEIN

; FILE REFERENCE: 210147.00XX/5U1

; CURRENT APPLICATION NUMBER: US/10/029,191

; CURRENT FILING DATE: 2001-12-20

; PRIOR APPLICATION NUMBER: 09/569,978

; PRIOR FILING DATE: 2000-05-12

; PRIOR APPLICATION NUMBER: US 60/134,198

; PRIOR FILING DATE: 1999-05-14

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 21

; LENGTH: 645


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; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2632
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-22

Alignment Scores:
Pred. No.: 4,49e-140 Length: 2632
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservatives: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-029-191-22 (1-2632)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 78 ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGCTCATCTACTGCGGTGAGA 137

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 138 GTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGACAGAGCGGTGCAGGGCAATCCC 197

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 198 ATGAAGCTGAGGTGCATCTCTGTCATGAAGAGGAGGAGGTGGAGGCCACCATCTGTGTG 257

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 258 CAGTGGTTCTACAGCCCTGAGGCGGTAAAGATTTCCTTATATAGTATCGGAATGGC 317

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 318 CACCAGGAAGTGGAGAGCCCTTCCAGGCCGTCTGCAGTGGATGGGAGCAAGACCTG 377

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 378 CAGGACGTATCCATCACTGCTACTCAATGTCACTTTGAATGACTCTGGCTCTACACATGC 437

Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 438 AATGTGTCAGGAGTTCGAATTCGAGGCACACAGGCCCTTTTGTGAAGACCAAGACTG 497

Qy 141 IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 498 ATACCTTTGCGAGTCACTGAAGAGCGGAGAGACTTCACCTCGTGGTCTCGGAATC 557

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180
Db 558 ATGATGTACATCCTCCTGCTTCTCACCCTTGCGCTGTTTATTGAGATGATCTATTGCT 617

Qy 181 TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 618 TACAGAAAGGTCTCTAAGGCCGAGAGGACACAGGAAATGCGTCTGACTACCTTGTCT 677

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 678 ATCCCTTCAGAGAACAGAGAACTCTGTGGTACCCTGTGGAGGAA 722

RESULT 6
US-10-029-191-1
; Sequence 1, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.

; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5UI
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3108
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-1

Alignment Scores:
Pred. No.: 5,81e-140 Length: 3108
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservatives: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-029-191-1 (1-3108)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 78 ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGCTCATCTACTGCGGTGAGA 137

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 138 GTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGACAGAGCGGTGCAGGGCAATCCC 197

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 198 ATGAAGCTGAGGTGCATCTCTGTCATGAAGAGGAGGAGGTGGAGGCCACCATCTGTGTG 257

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 258 GAGTGGTTCTACAGCCCTGAGGCGGTAAAGATTTCCTTATATAGTATCGGAATGGC 317

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 318 CACCAGGAAGTGGAGAGCCCTTCCAGGCCGTCTGCAGTGGATGGGAGCAAGACCTG 377

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 378 CAGGACGTATCCATCACTGCTACTCAATGTCACTTTGAATGACTCTGGCTCTACACATGC 437

Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 438 AATGTGTCAGGAGTTCGAATTCGAGGCACACAGGCCCTTTTGTGAAGACCAAGACTG 497

Qy 141 IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 498 ATACCTTTGCGAGTCACTGAAGAGCGGAGAGACTTCACCTCGTGGTCTCGGAATC 557

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180
Db 558 ATGATGTACATCCTCCTGCTTCTCACCCTTGCGCTGTTTATTGAGATGATCTATTGCT 617

Qy 181 TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 618 TACAGAAAGGTCTCTAAGGCCGAGAGGACACAGGAAATGCGTCTGACTACCTTGTCT 677

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 678 ATCCCTTCAGAGAACAGAGAACTCTGTGGTACCCTGTGGAGGAA 722

RESULT 7
US-10-450-763-22568
```

; Sequence 22568, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22568
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (518)..(1051)
; OTHER INFORMATION: 91% homologous to Homo sapiens voltage-gated sodium channel
; OTHER INFORMATION: beta-3 subunit, accession number AJ243396, Smith-Waterman Score=826
US-10-450-763-22568

Alignment Scores:
Pred. No.: 3,17e-116 Length: 1195
Score: 927.50 Matches: 184
Percent Similarity: 94.42% Conservative: 2
Best Local Similarity: 93.40% Mismatches: 9
Query Match: 82.52% Indels: 2
DB: 9 Gaps: 1

US-09-977-579A-2 (1-215) x US-10-450-763-22568 (1-1195)

Qy	1	MetProLalaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer	20
Db	463	ATGCCTGCCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGCTTATCTACTAGTCAGT	522
Qy	21	ValCysPheProValCysValGlu-ValProSerGluThrGluAla---ValGlnGlyAs	39
Db	523	GTCTGCTTCCCTGTGTGGGGGGAAGTGCCCTTAGAAAAAGGGGGGGCAGCGGTAA	582
Qy	39	nProMetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrVa	59
Db	583	CCCCATGAAGTCGCTGCATCTCTCTCATGAAGAGAGAGAGGTGGAGGCCACACGGT	642
Qy	59	lValGluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAs	79
Db	643	GGTGAATGGTTCTACAGGCCGAGGGCGGTAAAGATTTCCTATTATTCAGGATATCGAA	702
Qy	79	nGlyHisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAs	99
Db	703	TGGCCACACAGAGGTGGAGAGCCCTTTTCAGGGGCGCTTCAGTGGGAATGGCAACAAGA	762
Qy	99	pLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrTh	119
Db	763	CCTCAGAGACGTGTCATCACTGTGCTCAAGCTCACTCTGAACGACTCTGGCCCTCTACAC	822
Qy	119	rCysAsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrAr	139
Db	823	CTGCAATGTGTCGGGGGTTTGATTGTAGGGCGCATCGGCCCTTTGTGAAGACGACGC	882
Qy	139	gLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGl	159
Db	883	GCTGATCCCCCTAAGAGTACCGAGGAGGCTGGAGAGGACTTCACCTCTGTGGTCTCAGA	942
Qy	159	uIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTy	179
Db	943	AATCATGATGATACATCCTTCTGGTCTTCCCTCACCTTGTGGCTGCTCATCGAGATGATATA	1002

Qy	179	rCysTyrArgLysValSerLysAlaGluGluAlaAlaGlnGlnGluAsnAla	195
Db	1003	TTGCTACAGACAGGTCTCAAAAGCCGAAGAGGAGGCCCAAGAAACGCG	1051

RESULT 8

US-10-450-763-22567
; Sequence 22567, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22567
; LENGTH: 3531
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (300)..(407)
; OTHER INFORMATION: 94% homologous to Homo sapiens putative kruppel-related zinc
; OTHER INFORMATION: finger protein NY-REN-23 antigen, accession number AF155101, Smith-
; OTHER INFORMATION: Waterman Score=180.
US-10-450-763-22567

Alignment Scores:
Pred. No.: 2e-83 Length: 3531
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 61.74% Indels: 0
DB: 9 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-450-763-22567 (1-3531)

Qy	19	ValSerValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGly	38
Db	2959	GTCAAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGAGGAGCGGTGAGGGC	3018
Qy	39	AsnProMetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThr	58
Db	3019	AACCCCATGAAGCTGGCTGCATCTCTGCATGAAGAGAGAGAGGTGGAGGCCACACG	3078
Qy	59	ValValGluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArg	78
Db	3079	GTGGTGAATGGTTCTACAGCCCGAGGGCGGTAAAGATTTCCTATTATTCAGGATATCGG	3138
Qy	79	AsnGlyHisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLys	98
Db	3139	AATGGCCACACAGAGGTGGAGAGCCCTTTTCAGGGGCGCTTCAGTGAATGGCAGCAG	3198
Qy	99	AspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyr	118
Db	3199	GACCTGCAGGACGTGTCATCACTCACTCAAGTCACTCTGAACGACTCTGGCCTCTAC	3258
Qy	119	ThrCysAsnValSerArgGluPheGluAlaHisArgProPheValLysThrThr	138
Db	3259	ACCTGCAATGTGTCGGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGAAGACGACG	3318
Qy	139	ArgLeuIleProLeuArgValThrGluGlu	148
Db	3319	CGGCTGATCCCTTACAGATCACCGAGGAG	3348

RESULT 9

US-11-060-756-2816
; Sequence 2816, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2816
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2816
Alignment Scores:
Pred. No.: 1.98e-71 Length: 600
Score: 598.00 Matches: 119
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.20% Indels: 0
DB: 10 Gaps: 0
US-09-977-579A-2 (1-215) x US-11-060-756-2816 (1-600)
Qy 97 SerLyAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 3 AGCAAGGACCTGCAGGACGTGCTCACTGCTCAACGTCACCTCTGAAACGACTCTGGC 62
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPheVallys 136
Db 63 CTCTACACCTGCAATGTCCTCCGGAGTTTGAGTTTGAGGGGCATCGGCCCTTTGTGAAG 122
Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Db 123 ACGACGGCGCTGATCCCTTAAGAGTCACCGAGGAGCTGGAGAGGACTTCACCTCTGTG 182
Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuLeuIleGlu 176
Db 183 GTCTCAGAAATCATGATGTATCATCTCTGCTCTTCCCTCACCCTGTGGCTCATCGAG 242
Qy 177 MetIleTyrCysTyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSer 196
Db 243 ATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGCGTCT 302
Qy 197 AspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 303 GACTACCTTGCCATCCCATCTGAGAACAGGAGAACTCTGCGGTACCAAGTGGAGGAA 359
RESULT 10
US-11-060-756-2817
; Sequence 2817, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2817
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2817
Alignment Scores:
Pred. No.: 1.98e-71 Length: 600
Score: 598.00 Matches: 119
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.20% Indels: 0
DB: 10 Gaps: 0
US-09-977-579A-2 (1-215) x US-11-060-756-2817 (1-600)
Qy 97 SerLyAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 3 AGCAAGGACCTGCAGGACGTGCTCACTGCTCAACGTCACCTCTGAAACGACTCTGGC 62
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPheVallys 136
Db 63 CTCTACACCTGCAATGTCCTCCGGAGTTTGAGTTTGAGGGGCATCGGCCCTTTGTGAAG 122
Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Db 123 ACGACGGCGCTGATCCCTTAAGAGTCACCGAGGAGCTGGAGAGGACTTCACCTCTGTG 182
Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuLeuIleGlu 176
Db 183 GTCTCAGAAATCATGATGTATCATCTCTGCTCTTCCCTCACCCTGTGGCTCATCGAG 242
Qy 177 MetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSer 196
Db 243 ATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGCGTCT 302
Qy 197 AspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 303 GACTACCTTGCCATCCCATCTGAGAACAGGAGAACTCTGCGGTACCAAGTGGAGGAA 359

Alignment Scores:
Pred. No.: 1.98e-71 Length: 600
Score: 598.00 Matches: 119
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.20% Indels: 0
DB: 10 Gaps: 0
US-09-977-579A-2 (1-215) x US-11-060-756-2817 (1-600)
Qy 97 SerLyAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 3 AGCAAGGACCTGCAGGACGTGCTCACTGCTCAACGTCACCTCTGAAACGACTCTGGC 62
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPheVallys 136
Db 63 CTCTACACCTGCAATGTCCTCCGGAGTTTGAGTTTGAGGGGCATCGGCCCTTTGTGAAG 122
Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Db 123 ACGACGGCGCTGATCCCTTAAGAGTCACCGAGGAGCTGGAGAGGACTTCACCTCTGTG 182
Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuLeuIleGlu 176
Db 183 GTCTCAGAAATCATGATGTATCATCTCTGCTCTTCCCTCACCCTGTGGCTCATCGAG 242
Qy 177 MetIleTyrCysTyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSer 196
Db 243 ATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGCGTCT 302
Qy 197 AspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 303 GACTACCTTGCCATCCCATCTGAGAACAGGAGAACTCTGCGGTACCAAGTGGAGGAA 359
RESULT 11
US-11-060-756-7088
; Sequence 7088, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7088
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7088
Alignment Scores:
Pred. No.: 1.98e-71 Length: 600
Score: 598.00 Matches: 119
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.20% Indels: 0
DB: 10 Gaps: 0
US-09-977-579A-2 (1-215) x US-11-060-756-7088 (1-600)
Qy 97 SerLyAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 3 AGCAAGGACCTGCAGGACGTGCTCACTGCTCAACGTCACCTCTGAAACGACTCTGGC 62
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPheVallys 136
Db 63 CTCTACACCTGCAATGTCCTCCGGAGTTTGAGTTTGAGGGGCATCGGCCCTTTGTGAAG 122
Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156


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Db 123 ACGACGGCGGTGATCCCCCTAAGAGTCACCGAGGAGCTGGAGAGGACTTCACCTCTGTG 182
Qy 157 ValSerGluLeuMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuLeuGlu 176
Db 183 GTCTCAGAAATCATGATGTACATCTTCTGGTCTTCCTCACCCTGTGGCTGCTCATCGAG 242
Qy 177 MetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAAsnAlaSer 196
Db 243 ATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGAGCCCAAGAAAGACGCGTCT 302
Qy 197 AspTyrLeuAlaIleProSerGluAAsnLysGluAAsnSerAlaValProValGluGlu 215
Db 303 GACTACCTTGCCATCCATCTGAGAACAGAGAACTCTGCGGTACCAAGTGGAGGAA 359

RESULT 12
US-11-060-756-7089
; Sequence 7089, Application US/11060756
; Publication No. US200502213541
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7089
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7089

Alignment Scores:
Pred. No.: 1,98e-71 Length: 600
Score: 598.00 Matches: 119
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.20% Indels: 0
DB: 10 Gaps: 0

US-09-977-579A-2 (1-215) x US-11-060-756-7089 (1-600)
Qy 97 SerLysAspLeuGlnAspValSerIleThrValLeuAAsnValThrLeuAAsnSerGly 116
Db 3 AGCAAGGACCTGCGAGGAGTGTCTCATCTGCTGCTCAACGTCACTCTGAAGACTCTGGC 62
Qy 117 LeuTyrThrCysAAsnValSerArgGluPheGluPheGluAlaHisArgProPheValLys 136
Db 63 CTCTACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGAAG 122
Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Db 123 ACGACGGCGGTGATCCCCCTAAGAGTCACCGAGGAGCTGGAGAGGACTTCACCTCTGTG 182
Qy 157 ValSerGluLeuMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuLeuGlu 176
Db 183 GTCTCAGAAATCATGATGTACATCTTCTGGTCTTCCTCACCCTGTGGCTGCTCATCGAG 242
Qy 177 MetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAAsnAlaSer 196
Db 243 ATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGAGCCCAAGAAAGACGCGTCT 302
Qy 197 AspTyrLeuAlaIleProSerGluAAsnLysGluAAsnSerAlaValProValGluGlu 215
Db 303 GACTACCTTGCCATCCATCTGAGAACAGAGAACTCTGCGGTACCAAGTGGAGGAA 359

RESULT 13
US-10-029-191-23
; Sequence 23, Application US/10029191
; Publication No. US20020160453A1
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```
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Lepus Sp.
US-10-029-191-23

Alignment Scores:
Pred. No.: 9,49e-55 Length: 657
Score: 477.00 Matches: 106
Percent Similarity: 64.49% Conservative: 32
Best Local Similarity: 49.53% Mismatches: 68
Query Match: 42.44% Indels: 8
DB: 5 Gaps: 5

US-09-977-579A-2 (1-215) x US-10-029-191-23 (1-657)
Qy 10 LeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCysValGluVal 29
Db 13 CTGGCTTTCTGGTGTGGCGCGCGCTGTCTCGGCCCTGGGGGGCTCGGTGGAGGTG 72
Qy 30 ProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMet 49
Db 73 GACTCGAGACCGAGCCGTGTACGGGATGACCTTCANAATTCTGTGCATCTCTCTGCAAG 132
Qy 50 LysArgGluGluValGluAlaThrValValGluTrpPheTyrArgProGluGlyGly 69
Db 133 CGCGCGGACGAGACACCGCGCGAGACCTTCACGAGTGGACCTTCGCCCAAGAGGGCACT 192
Qy 70 LysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGlnGluValGluSerPro--- 87
Db 193 GAGGAGTTCGTCAAGATCTCTGCGCTATGAGACGAGGTGCTGAGAGGAGAGACGAG 252
Qy 88 ---PheGlnGlyArgLeuGlnTrpAsnGlySer-----LysAspLeuGlnAspVal 103
Db 253 CGCTTTGAGGCGCGGTGTGTGGACGCGCGCGGACCAAGGACCTTCGAGGACCTG 312
Qy 104 SerIleThrValLeuAAsnValThrLeuAAsnAspSerGlyLeuTyrThrCysAAsnValSer 123
Db 313 TCCATCTTCATCACCATGTCACTACACCACTCGCGGCGACTACCAAGTGCCTGTCTAC 372
Qy 124 ArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeuIleProLeu 143
Db 373 CGCTGCTCTCTCTCGAAAACACTACGAGCACACACCGAGCGTCTGCAAGAGATCCACCTG 432
Qy 144 ArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIleMetMetTyr 163
Db 433 GAGGTGTGGACCAAGGCCAACAGACATGGCATCTCATCTGTCGGGAGATCATGATGTAC 492
Qy 164 IleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCysTyrArgLys 183
Db 493 GTGCTCATCGTGGTGTGACCATCTGGCTCGTGGCGAGATGGTGTGTACTCTCTACCAAG 552
Qy 184 ValSerLysAla---GluGluAlaAlaGlnGluAAsnAlaSerAspTyrLeuAlaIlePro 202
Db 553 ATCGCGCGCGCGGAGGAGGCGGCGGAGAGACGCTTCGGAATACTTTGGCCATCACC 612
Qy 203 SerGluAAsnLysGluAAsn---SerAlaValProValGluGlu 215
Db 613 TCAGAAAGCAAGAAATAATTCACGGGCGTCCAGGCTGCTGAA 654
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RESULT 14
US-10-723-860-2247
; Sequence 2247, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziiz, Nataasha
; APPLICANT: Zlotnik, Albert
; APPLICANT: Ginsburg, Wendy M.
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 03682.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723.860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2247
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2247

Alignment Scores:
Pred. No.: 1.01e-53 Length: 1335
Score: 473.00 Matches: 109
Percent Similarity: 63.35% Conservative: 31
Best Local Similarity: 49.32% Mismatches: 71
Query Match: 42.08% Indels: 10
DB: Gaps: 6

US-09-977-579A-2 (1-215) x US-10-723-860-2247 (1-1335)

Qy 3 AlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCys 22
Db 22 GCCATGGGGAGGCTG-----CTGGCTTAGTGTGGCGCGGCACCTGGTCTCTCAGCC 75
Qy 23 PheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLys 42
Db 76 TCGGGGGCTCGTGGAGGTGACTCGGAGACCGAGCCGCGTGTGGATGACCTTCAA 135
Qy 43 LeuArgCysIleSerCysMetLysArgGluValGluAlaThrValValGluTrp 62
Db 136 ATTTCTTCATCTCTCTGCAAGCGCGCAGCGACCAACGCTGAGACCTTCAACGAGTGG 195
Qy 63 PheTyrArgProGluGlyGlyAspPheLeu---IleTyrGluTyrArgAsnGlyHis 81
Db 196 ACCTTCCGCCAAGAGGCACTGAGGAGTTTGTCAAGATCCTCGCGCTATGAGAATGAGGTG 255
Qy 82 GlnGluValGluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer----- 97
Db 256 TTGCAGCTGGAGGAGGATGAGCGCTTCAGGGCGCGTGGTGGAAATGGCAGCGCGGGC 315
Qy 98 ---LysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 316 ACCAAGACCTGCAGGATCTGTATCTTCATCACCATGTCACTACACCACTCGGGC 375
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPheValLys 136
Db 376 GACTACGAGTGCACGCTACCGCTGTCTTCTTCGAAAACTACGACGACCAACACCAAGC 435
Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Db 436 GTGCTCAAGAAGATCCACATGAGGTAGTGACAAAGCCCAACAGAGATCGGCATCCATC 495
Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGlu 176
Db 496 GTGCTGAGATCATGATGATGCTCATTTGTGGTTGTGACCATATGCTCGTGCACAG 555
Qy 177 MetIleTyrCysTyrArgLysValSerLysAla---GluGluAlaAlaGlnGluAsnAla 195
Db 556 ATGATTTACTGTACAAGAAGATCGTCCGCCCGCAGGAGCTGCTGCACAGGAATGCC 615

Qy 196 SerAspTyrLeuAlaIleProSerGluAsnLysGluAsn---SerAlaValProValGlu 214
Db 616 TCGGAATACCTGGCCATCACTCTGAAAGCAAGAGAACTGCACGGCGCTCCAGGTGGCC 675
Qy 215 Glu 215
Db 676 GAA 678
RESULT 15
US-10-477-272-1
; Sequence 1, Application US/10477272
; Publication No. US20040191791A1
; GENERAL INFORMATION:
; APPLICANT: Biomedics Limited
; TITLE OF INVENTION: P12
; FILE REFERENCE: SCN1B (R85C)
; CURRENT APPLICATION NUMBER: US/10/477,272
; CURRENT FILING DATE: 2003-11-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-272-1

Alignment Scores:
Pred. No.: 1.1e-53 Length: 1414
Score: 473.00 Matches: 109
Percent Similarity: 63.35% Conservative: 31
Best Local Similarity: 49.32% Mismatches: 71
Query Match: 42.08% Indels: 10
DB: Gaps: 6

US-09-977-579A-2 (1-215) x US-10-477-272-1 (1-1414)

Qy 3 AlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCys 22
Db 98 GCCATGGGGAGGCTG-----CTGGCTTAGTGTGGCGCGGCACCTGGTCTCTCAGCC 151
Qy 23 PheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLys 42
Db 152 TCGGGGGCTCGTGGAGGTGACTCGGAGACCGAGCCGCGTGTGGATGACCTTCAA 211
Qy 43 LeuArgCysIleSerCysMetLysArgGluValGluAlaThrValValGluTrp 62
Db 212 ATTTCTTCATCTCTCTGCAAGCGCGCAGCGACCAACGCTGAGACCTTCAACGAGTGG 271
Qy 63 PheTyrArgProGluGlyGlyAspPheLeu---IleTyrGluTyrArgAsnGlyHis 81
Db 272 ACCTTCCGCCAAGAGGCACTGAGGAGTTTGTCAAGATCCTCGCGCTATGAGAATGAGGTG 331
Qy 82 GlnGluValGluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer----- 97
Db 332 TTGCAGCTGGAGGAGGATGAGTGTCTCGAGGGCGCGTGGTGGAAATGGCAGCGCGGGC 391
Qy 98 ---LysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 392 ACCAAGACCTGCAGGATCTGTATCTTCATCACCATGTCACTACACCACTCGGGC 451
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPheValLys 136
Db 452 GACTACGAGTGCACGCTACCGCTGTCTTCTTCGAAAACTACGACGACCAACACCAAGC 511
Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Db 512 GTGCTCAAGAAGATCCACATGAGGTAGTGACAAAGCCCAACAGAGATCGGCATCCATC 571
Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGlu 176
Db 572 GTGCTGAGATCATGATGATGCTCATTTGTGGTTGTGACCATATGCTCGTGCAGAG 631
Qy 177 MetIleTyrCysTyrArgLysValSerLysAla---GluGluAlaAlaGlnGluAsnAla 195

Db 632 ATGATTACTCTCAAGAGATCGTCCGCCACGGAGACTGCTGCACAGAGAAATGCC 691
 Qy 196 SerAspTyrLeuAlaIleProSerGluAsnLysGluAsn---SerAlaValproValGlu 214
 Db 692 TCGGAATACCTGGCCATCACCTCTGAAGCAAGAGAACTGCACGGGGCGTCCAGTG GCC 751
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 Db 752 GAA 754

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GenCore version 5.1.6
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Perfect score: 1124

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DLOCALIGN=200 -THR SCORE=pct -THR MAX=100
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Database :

Published Applications NA New:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1124	100.0	1261	6	US-10-374-954-8
2	473	42.1	1335	6	US-10-374-954-4
3	241	21.4	880	6	US-10-750-185-44336
4	165.5	14.7	150468	7	US-11-112-908-56
5	165.5	14.7	193789	7	US-11-112-908-55
6	147	13.1	673	7	US-11-080-991-111
7	147	13.1	1371	6	US-10-131-826A-487
8	131	11.7	1777	6	US-10-131-826A-529

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Score: 100.00%
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Length: 1261
Matches: 215
Conservative: 0
Mismatch: 0
Indels: 0

ALIGNMENTS

RESULT 1

US-10-374-954-8
; Sequence 8, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (376)..(1023)
US-10-374-954-8

Sequence 6, Appli
Sequence 519, App
Sequence 387, App
Sequence 44339, A
Sequence 80, Appl
Sequence 44343, A
Sequence 62, Appl
Sequence 367, App
Sequence 30397, A
Sequence 367, App
Sequence 13, Appl
Sequence 31, Appl
Sequence 77, Appl
Sequence 8, Appli
Sequence 7, Appli
Sequence 48, Appl
Sequence 516, App
Sequence 60713, A
Sequence 27, Appl
Sequence 44, Appl
Sequence 6, Appli
Sequence 83, Appli
Sequence 1, Appli
Sequence 39, Appl
Sequence 37, Appl
Sequence 156, App
Sequence 158, App
Sequence 7, Appli
Sequence 94, Appl
Sequence 45, Appl
Sequence 95, Appl
Sequence 242, App
Sequence 95, Appl
Sequence 36, Appl
Sequence 96, Appl
Sequence 42, App

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DB: 6 Gaps: 0
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Dy 376 ATGCTGCTCCTCAATAGATTGTTTCCCTGCTGCTCTCTCGTGTATCTACTAGGGTCAGT 435
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Dy 436 GTCTGCTTCCCTGCTGTGTGTGAAGTGCCTTCGAGACGGAGCGCTGCAGGGCAACCC 495
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal 60
Dy 496 ATGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 555
Qy 61 GluTrpPheTyrArgProGluGlyCysLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Dy 556 GAATGGTTCACAGCGCGAGCGCGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 615
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Dy 616 CACCAGGAGGTGGAGAGCGCTTTTCAGGGCGCGCTGAGTGGAAATGGCAGCAGGACCTG 675
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Dy 676 CAGACGTGCTCCATCAGTGTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 735
Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Dy 736 AATGTGTCCTGGAGTTTGTAGTTTGGAGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 795
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValSerGluIle 160
Dy 796 ATCCCTTAAGAGTCAACGAGGAGCTGGAGAGGACTTCACCTCTGTGTGTCTCAGAAATC 855
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Dy 856 ATGATGATACATCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 915
Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAlaGlnGluAlaSerAspTyrLeuAla 200
Dy 916 TACAGAAAGGTCTCAAAAGCCGAGAGAGCGCCCAAGAAACGCGTCTGACTACCTTGCC 975
Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Dy 976 ATCCCATCTGAGAACAGGAGAACTCTCGGTACCAGTGGAGAA 1020
RESULT 2
US-10-374-954-4
; Sequence 4, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L.
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
; FILE REFERENCE: 1242/41/2
; CURRENT FILING DATE: US/10/374,954
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(681)
US-10-374-954-4
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Alignment Scores:
Pred. No.: 2,79e-52 Length: 1335
Score: 473.00 Matches: 109
Percent Similarity: 63.35% Conservatives: 31
Best Local Similarity: 49.32% Mismatches: 71
Query Match: 42.08% Indels: 10
DB: 6 Gaps: 6
US-09-977-579A-2 (1-215) x US-10-374-954-4 (1-1335)
Qy 3 AlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCys 22
Dy 22 GCCATGGGGAGGGCTG-----CTGGCCTTAGTGTGCGCGCGGACCTGGTGTCTCTCAGCC 75
Qy 23 PheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLys 42
Dy 76 TGGCGGGGGCTGCGTGGAGGTGGACTCGAGACCGGAGCGCTGATGGATGACCTTCAAA 135
Qy 43 LeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValValGluTrp 62
Dy 136 ATTCTTTGCACTCTCTGCAAGCGCGGAGGACCAACGCTGAGACCTTCACCGATGG 195
Qy 63 PheTyrArgProGluGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHis 81
Dy 196 ACCTTCGCCAGAGGAGGAGGAGGAGGAGTGTCAAGATCTCTGCGCTATGAGATGAGGTG 255
Qy 82 GlnGluValGluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer----- 97
Dy 256 TTGCAGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 315
Qy 98 ---LysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Dy 316 ACCAAGACCTTGAGGATCTCTATCTTCTATCACCAGTGTACCTACCAACCACTCGGCG 375
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPheValLys 136
Dy 376 GACTACGAGTGCCACGCTACCGCGCTCTCTTTCGAAACATACGAGGACCAACCCAGC 435
Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Dy 436 GTCGTCAAGAGATCCACATTTGAGGTAGTGACACCAAGCCCAACAGAGACATGGCATCC 495
Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGlu 176
Dy 496 GTGCTCGAGATCATGATGATGCTATGCTATGCTGTTGTTGACCATATGGCTCTGGCAGAG 555
Qy 177 MetIleTyrCysTyrArgLysValSerLysAla---GluGluAlaAlaGlnGluAsnAla 195
Dy 556 ATGATTTACTGTACAAAGATCGCTGCCCGCCACGAGAGACTGCTGCACAGGAGAAATGCC 615
Qy 196 SerAspTyrLeuAlaIleProSerGluAsnLysGluAsn---SerAlaValProValGlu 214
Dy 616 TCGGAATACCTGGCCATCACCCTCTGAAAGCAAGAGAACTGCACGGGCGTCCAGGTGGCC 675
Qy 215 Glu 215
Dy 676 GAA 678
RESULT 3
US-10-750-185-44336
; Sequence 44336, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
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Db 108996 GAAGAGGATTCATTATTTTACAAATTTGAAGAAACAGAGG-----CCTAGAGACATTTGAGTC 109049
Qy 86 rProPheGlnGlyArgLeu-----GlnTrp-----AenGlySerLysAs 99
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Qy 99 pLeuGlnAspValserIle-----ThrValLeuAsnValThrLeuAsnAspSerGlyLe 117
Db 109110 GGTTCAGAGCTACCGCTTTTAGGCACCGTCTGAGGGCCCTCCAG-AATGACACAGATGT 109168
Qy 117 uTyThrCysAsnValSerArgGluPheGluPheGluAlaHisArg----- 132
Db 109169 GGCCTCGAGTTACACAGGCGCAGGTTGAGGGTGACCCACCAGCGGCTACCCAAAGGCT 109228
Qy 133 -----ProPheValLysThrThrArgLeuProLeu----- 143
Db 109229 GGGTATTAAATACAGTGCATACACAGGCCCGCAGGAGGTGAGCCATCATCCCAAGC 109288
Qy 143 ----- 143
Db 109289 TCACACGAAGCTCACAGCACTCAGGCTGTCTATGCAGCGCTGGGCTACCCCTTAACC 109348
Qy 144 -ArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIleMetMetTy 163
Db 109349 CTGCCTGGCCCTGCAGGCCAACAGAGACATGGCATCCATCGTGTCTGAGATCATGATGA 109408
Qy 163 rIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyCysTyArgLy 183
Db 109409 TGTGCTCATTTGGTGTGACCATATGCTCGTGGCAGAGATGATTACTGCTACAAGAA 109468
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RESULT 6
US-11-080-991-111
; Sequence 111, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-080-991-111

Alignment Scores:
Pred. No.: 2.38e-09 Length: 673
Score: 147.00 Matches: 57
Percent Similarity: 41.44% Conservative: 35
Best Local Similarity: 25.68% Mismatches: 80
Query Match: 13.08% Indels: 50
Db: 7 Gaps: 9

US-09-977-579A-2 (1-215) x US-11-080-991-111 (1-673)
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Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 131 -----CTGAGGCTGTTAATGGACAGATGCTCGGTAAATGCACT 172
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Qy 160 IleMetMetTyTrpIleLeuLeuVal-----PheLeuThrLeuTrpLeu 173
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Db 539 GTAGTGTCTCTCTCCAGCATTTACCGGAAAAAGCGATGGGCGGAAAGAGCT----- 589
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; Sequence 487, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deanoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 487
; LENGTH: 1371
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-487

Alignment Scores:
Pred. No.: 7.13e-09 Length: 1371
Score: 147.00 Matches: 57
Percent Similarity: 41.44% Conservative: 35
Best Local Similarity: 25.68% Mismatches: 80
Query Match: 13.08% Indels: 50
DB: 6 Gaps: 9

US-09-977-579A-2 (1-215) x US-10-131-826A-487 (1-1371)

Qy 7 LeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCys 26
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 CTITGGCTATAGCAGCT---GTGGAATTTATACCTCCCGGGTG-----222

Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysValle 46
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
223 -----CTGGAGGCTGTTAATGGGACAGATGCTCGGTTAAATGCACT 264

Qy 47 SerCysMetLysArgGluGluValGluAlaThrThrValValGluTrpPheTyrArgPro 66
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
265 TTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACC---TGGAATTTTCGTCT 321

Qy 67 ---GluGlyGly---LysAspPheLeuIleTyrGluTyrArgAsnGlyHisGlnGluVal 84
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
322 CTAGACGGGGACCTGAGCAGTTGTATTCTTACTACCATAGATGATCCCTTCCACCCCATG 381

Qy 85 GluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeuGlnAspValSer 104
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
382 AGTGGCGGTTTAGGACCGGGTGTCTTGGATGGGAATCCTGAGCGGTACGATGCTCTCC 441

Qy 105 IleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSerArg 124
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
442 ATCTCTCTCGAAACTTCAGTTCGACGACAAATGGGACATACACCTGCCAGGTGAAGAAC 501

Qy 125 GluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeuIleProLeuArg 144
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
502 -----CCACCTGAT 510

Qy 145 ValThrGluGluAlaGlyGluAspPheThrSerValVal-----SerGlu 159
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
511 GTTGATGGGTGATAGGGGAGATCCGGCTCAGCGTCTGTCGACACTGATCGCTTCTCTGAG 570

Qy 160 IleMetMetTyrIleLeuLeuVal-----PheLeuThrLeuTrpLeu 173
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
571 ATCCACTCTCGGCTCTGGCCATTGGCTCTGCCCTGTGCACTGATGATCATAAGTAATT 630

Qy 174 LeuIleGluMetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaGlnGlu 193
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
631 GTATGTGCTCTCTTCCAGCATTTACCGGAAAGAGATGGGCCCGAAGAGCT-----681

Qy 194 AsnAlaSerAspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProVal 213
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
682 -----CATAAAGTGGTGAGATAAAATCAAAAGAGAGAAAGGCTCAACCAA 729

Qy 214 GluGlu 215
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
730 GAGAAA 735

RESULT 8
US-10-131-826A-529
; Sequence 529, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 529
; LENGTH: 1777
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-529

Alignment Scores:
Pred. No.: 1.43e-06 Length: 1777
Score: 131.00 Matches: 51
Percent Similarity: 37.39% Conservative: 32
Best Local Similarity: 22.97% Mismatches: 81
Query Match: 11.65% Indels: 58
DB: 6 Gaps: 9

US-09-977-579A-2 (1-215) x US-10-131-826A-529 (1-1777)
```

```
Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 280 GTATATACCCCAAAAGAAATCTTCGTGCMAATGGTACACAAAGGGAAGCTGACCTGC--- 336
Qy 47 SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe 63
Db 337 -----AAGTTCAAGTCTACTAGTACGACTGGCGGTTGACCTCAGTCTCCTGGAGC 387
Qy 64 TyrArgProGluGlyLysAspPheLeu---lleTyrGluTyrArgAsnGlyHisGln 82
Db 388 TTCACGACAGAGGGCGGCACACTACTGTGTGCTGTTTTCCTACTCTCCAAAGGCAAGTG 447
Qy 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 448 TACCTTGGGAATTATCCACCAATTTAAAGACAGAATCAGCTGGCTGGAGACCTTGACAAG 507
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 508 AAAGATGCATCAATCAACATAGAAAATATCAGTATTATACACAATGGCACCTATATCTGT 567
Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 568 GATGTCAAAAC----- 579
Qy 141 IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValSerGlu--- 159
Db 580 ---CCTCTGACATCGTTGTCAGCTGCACACATTAGGCTCTATGTCGTAGAAAAAGAG 636
Qy 160 -----lleMetMetTyrIleLeuLeuValPheLeuThr 170
Db 637 AATTGGCTGTGTTCCAGTTTGGGTAGTGGTGGCATAGTTACTGTGTGGTCTTAGGT 696
Qy 171 LeuTrpLeuIleGluMetIleTyrCys-----TyrArgLys----- 183
Db 697 CTCACTGTCTCATCAGCATGATTCTGCTGCTCTCTATAGAGAAAAAACTCTAAACGG 756
Qy 184 -----ValSerLysAlaGluGluAlaAlaGlnGlu 193
Db 757 GATTACACTGGCTGCAGTACATCAGAGAGTTTGTCCACAGTTAAGCAGGCTCCTCGGAAG 816
Qy 194 AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer 209
Db 817 TCCCTCCGACACTGAGGGTCTTTGTAAGAGTCTGCTCTTCTGATCTCACCAGGGCCCA 876
Qy 210 AlaVal 211
Db 877 GTCATA 882

RESULT 9
US-10-374-954-6
; Sequence 6, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR FILING DATE: 2003-02-25
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(648)
US-10-374-954-6
```

```
Alignment Scores:
Pred. No.: 0.000162 Length: 648
Score: 110.50 Matches: 55
Percent Similarity: 45.33% Conservative: 42
Best Local Similarity: 25.70% Mismatches: 88
Query Match: 9.83% Indels: 29
DB: 6 Gaps: 11

US-09-977-579A-2 (1-215) x US-10-374-954-6 (1-648)

Qy 2 ProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerVal 21
Db 28 CCTGCTTCAGC-----CTCAGCGGGCTCAGTCTCTTTTC-----TCTTTG 69
Qy 22 CysPhePro-----ValCysValGluValProSerGluThrGluAlaValGlnGly 38
Db 70 GTGCCACAGAGGAGCATGGAGGTACAGTACTCTGCCACCTCCCAACGCTCTCAATGGC 129
Qy 39 AsnProMetLysLeuArgCysIle-----SerCysMetLysArgGluGluValGluAla 56
Db 130 TCTGACGCCGCTGCCCTGCACCTTCAACTCTCTGTACACAGTGAACACCAACAGTTC 189
Qy 57 ThrThrValValGluTrpPheTyrArgProGluGlyGly-----LysAspPheIleu 73
Db 190 TCC-----CTGAACCTGGACTTACCAGGAGTGCACAACTGCTCTGAGGAGATGTTCTC 243
Qy 74 IleTyrGluTyrArgAsnGlyHisGlnGluValGluSerProPheGlnGlyArgLeuGln 93
Db 244 CAGTTCGCGATGAAGATCATTAACCTGAGCTGAGCGGG-----TTTCAAGCCGCTGGAG 300
Qy 94 TrpAsnGlySerLysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsn 113
Db 301 TTCTCAGGAACCCCAAGTACGATGTGTGCGTGATGCTGAGAAACGTGCAGCCCGAG 360
Qy 114 AspSerGlyLeuTyrThrCysAsnValSerArgGluPheGluPheGluAlaHisArgPro 133
Db 361 GATGAGGGGATTTACAACTGCTACATCATGAAC-----CCCCCTGACCGCACCGTGGC 414
Qy 134 PheValLysThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPhe 153
Db 415 CATGGCAAG-----ATCCATCTGAGGTCTCTATGGAAGACCCCTGAGCGG 462
Qy 154 ThrSerValValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeu 173
Db 463 GACTCCACGGTGGCGGTGATTGTGGGTGCTCGCGGGCTTCTCTGGCTGTGTGTCTCATC 522
Qy 174 LeuIleGluMetIleTyr-----CysTyrArgLysValSerLysAlaGluGluAlaGln 192
Db 523 TTGGTGTGTGTGTGTGTCAGTGTGTGAGGAGA-----AAAAAAGAGCAG 567

Qy 193 GluAsnAlaSerAspTyrLeuAlaIleProSerGluAsnLys 206
Db 568 AAGCTGACACAGATGACCTGAAGACCGGAGGAGGGCGAAG 609

RESULT 10
US-10-131-826A-519
; Sequence 519, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
```

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; APPLICANT: Tamas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 519
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-519

Alignment Scores:
Pred. No.: 0.00106 Length: 1630
Score: 109.00 Matches: 47
Percent Similarity: 37.31% Conservative: 25
Best Local Similarity: 24.35% Mismatches: 85
Query Match: 9.70% Indels: 6
DB: 6 Gaps: 6

US-09-977-579A-2 (1-215) x US-10-131-826A-519 (1-1630)

Qy 16 IletYrTrpValSerValCysPheProValCysValGluValProSerGluThrGluAla 35
    :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 460 GTGTTCAAGAGCGCGGTGACTGCTCATGCTCCAGAGAGCGCCAAAGAGCTCATGGTC 519

Qy 36 ValGlnGlyAanProMetLysLeuArgCysIleSerCysMetLysArgGluGluValGlu 55
    :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 520 CATGTGGGTGGATTGATTCAGATGGGATGTT-----TTCAGACACAGAGTGGAAA 573

Qy 56 AlaThrThrValValGluTrpPheTyArgProGluGlyGlyLysAspPheLeuIleTy 75
    :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 574 CACGTGACCAAGGTAGATGATATTTTCAGGACGCGCGCAAGAGGAGGATGTTATT 633

Qy 76 GluTyArgAen-----GlyHisGlnGlu 83
    :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 634 CGTTACTACCACAACTCAGGATGCTGTGGAGTACTCCAGAGCTGGGGCCAC----- 687

Qy 84 ValGluSerProPheGlnGlyArgLeuGlnTrpAanGlySerLysAspLeuGlnAspVal 103
    :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 688 -----TTCAGAAATCGTGTAACCTGGTGGGGACATTTCCCGCAATGACGGT 735

Qy 104 SerIleThrValLeuAanValThrLeuAanAspSerGlyLeuTyThrCysAanValSer 123
    :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 736 TCCATCATGCTTCAAGAGGTGAGGAGTCAGATCGAGGAAACTACACTGCAGTATCCAC 795

Qy 124 -----ArgGluPheGluPheGluAlaHisArg 132
    :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::

```

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Db 796 CTAGGGAACCTGTGTTCAGAAAAACCATTTGCTGATGCTCAGCCCGGAGAGCCTCGA 855
Qy 133 ProPheValLysThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAsp 152
    :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 856 ACACCTGGTGACCCCGCAGCCCTGAGGCCTCTGGTCTTG-----GGTGGTAATCAG 906
    :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Qy 153 PheThrSerValValSerGluIleMetMetTyIleLeuLeuValPheLeuThrLeuTrp 172
    :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 907 TTGGTGATCATTTGGGAATTGCTGTGCCACAATCTGCTG-----CTCCCTGTTCTG 960
    :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Qy 173 LeuLeuIleGluMetIleTyCysTyArgLysValSer 185
    :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 961 ATATTGATCGTGAAGAGACCTGTGGAATAAGAGTTCA 999
    :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::

```

RESULT 11

```

US-10-131-826A-387
; Sequence 387, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 387
; LENGTH: 2458
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-387

```

```

Alignment Scores:
Pred. No.: 0.00233 Length: 2458
Score: 108.50 Matches: 51
Percent Similarity: 39.51% Conservative: 30

```

```
Best Local Similarity: 24.88% Mismatches: 69
Query Match: 9.65% Indels: 55
DB: 6 Gaps: 10

US-09-977-579A-2 (1-215) x US-10-131-826A-387 (1-2458)
Qy 18 TrpValSerValCysPheProValCysValGluValProSer----- 31
Db 550 TGGAGCCATGTCATCTAAAGTCTTAGTGAGA---CCATCCAAAGCCCAAGTGTGAGTTG 606
Qy 32 GluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMetLysArg 51
Db 607 GAAGAGAGCTGACAGAAAGGAGCTGACCTGACTTTGCAGTGTGAGTATCCTCTGGCACA 666
Qy 52 GluGluValGluAlaThrThrValValGluTrp---PheTyrArgProGluGlyGlyLys 70
Db 667 GAGCCCATTT-----GTATTACTGGCAGCGAATCCGAGAGAAAGAGGGAGAG 714
Qy 71 AspPheLeuIleTyrGluTyrArgAsnGlyHisGlnGluValGluSerProPheGlnGly 90
Db 715 GATGACGCTCTG-----CCTCCCAATCT 738
Qy 91 ArgLeuGlnTrpAsnGlySerLysAspLeuGlnAspValSerIleThrValLeuAsnVal 110
Db 739 AGGATTGACTACAAC-----CACCCCTGGCAGGTTCTGCTGCAGAAATCTT 783
Qy 111 ThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSerArgGluPheGluAla 130
Db 784 ACCATGTCTCTACTTGGACTGTACAGTGCACAGCAGCAACGAGCTGGGAAGGAAGC 843
Qy 131 HisArgProPheValLysThrArgLeuIleProLeuArgValThrGluAlaGly 150
Db 844 -----TGTGTGGTGCAGTAACGTACATATGTA 873
Qy 151 GluAspPheThrSerVal-----ValSerGluIleMetMetTyrIleLeuVal 167
Db 874 CAAAGCATCGCGATGTTGCAGGAGCAGTGCACAGCAGTGTGGTGGAGCCCTGCTGATT 933
Qy 168 PheLeuThrLeuTrpLeuLeuGluMetIleTyrCysTyrArgLysValSerLysAla 187
Db 934 TTCCTCTTGGTGGCTGCTAATC-----CGAAGGAAAGACAAAGAA 975
Qy 188 GluGluAlaAlaGlnAsnAlaSerAspTyrLeuAlaIleProSerGluAsnLysGlu 207
Db 976 AGATATGAGGAAGAGAGAGA-----CCTAATGAAATCGAGAA 1014
Qy 208 AsnSerAlaValPro 212
Db 1015 GATGCTGAAGCTCCA 1029

RESULT 12
US-10-750-185-44339
; Sequence 44339, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44339
; LENGTH: 1497
; TYPE: DNA

; ORGANISM: Bovine 19866880940727
US-10-750-185-44339
Alignment Scores:
Pred. No.: 0.00318 Length: 1497
Score: 105.00 Matches: 21
Percent Similarity: 95.45% Conservative: 0
Best Local Similarity: 95.45% Mismatches: 1
Query Match: 9.34% Indels: 0
DB: 6 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-750-185-44339 (1-1497)
Qy 194 AsnAlaSerAspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProVal 213
Db 1289 AACAGGCTCTGACTACCTGGCCATCCCATCGAGACAAAGAACTCTGCAGTCCCGAGTG 1348
Qy 214 GluGlu 215
Db 1349 GAGGAA 1354

RESULT 13
US-11-121-086-80
; Sequence 80, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80
; LENGTH: 138821
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-80
Alignment Scores:
Pred. No.: 7.33 Length: 138821
Score: 102.50 Matches: 31
Percent Similarity: 40.00% Conservative: 25
Best Local Similarity: 22.14% Mismatches: 63
Query Match: 9.12% Indels: 21
DB: 7 Gaps: 4

US-09-977-579A-2 (1-215) x US-11-121-086-80 (1-138821)
Qy 15 LeuIleTyrTrpValSerValCysPheProValCysValGluValProSerGluThrGlu 34
Db 47246 CTCCTTTTTCACAGTATCCAGCATGCTCAGAAAGTAACCAAGCGCAGACTGAAATTTCT 47305
Qy 35 AlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMetLysArgGluVal 54
Db 47306 GTGGTGGAGAGGAGGATGACCTTGGACTGTGTG-----TATGAAACCCGT 47353
Qy 55 GluAlaThrThrValValGluTrpPheTyrArgProGluGlyLysAspPheLeuIle 74
Db 47354 GATACTACTTATTACTTCTGTTACAGCAACCAACCAAGTGGAGAA-----TTGTTT 47407
Qy 75 TyrGluTyrArgAsnGlyHisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrp 94
Db 47408 TTCCTTTATTCGCGAACTCTTTTGTATGAGCAAAATGAAATGAGTGTGCGTATTTCTGG 47467
Qy 95 AsnGlySerLysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAsp 114
Db 47468 AACTTCCGAAATTCACACGAGTTCCTTCACTTCCATCACAGCTCACAGTGTGGAC 47527
Qy 115 SerGlyLeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPhe 134
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